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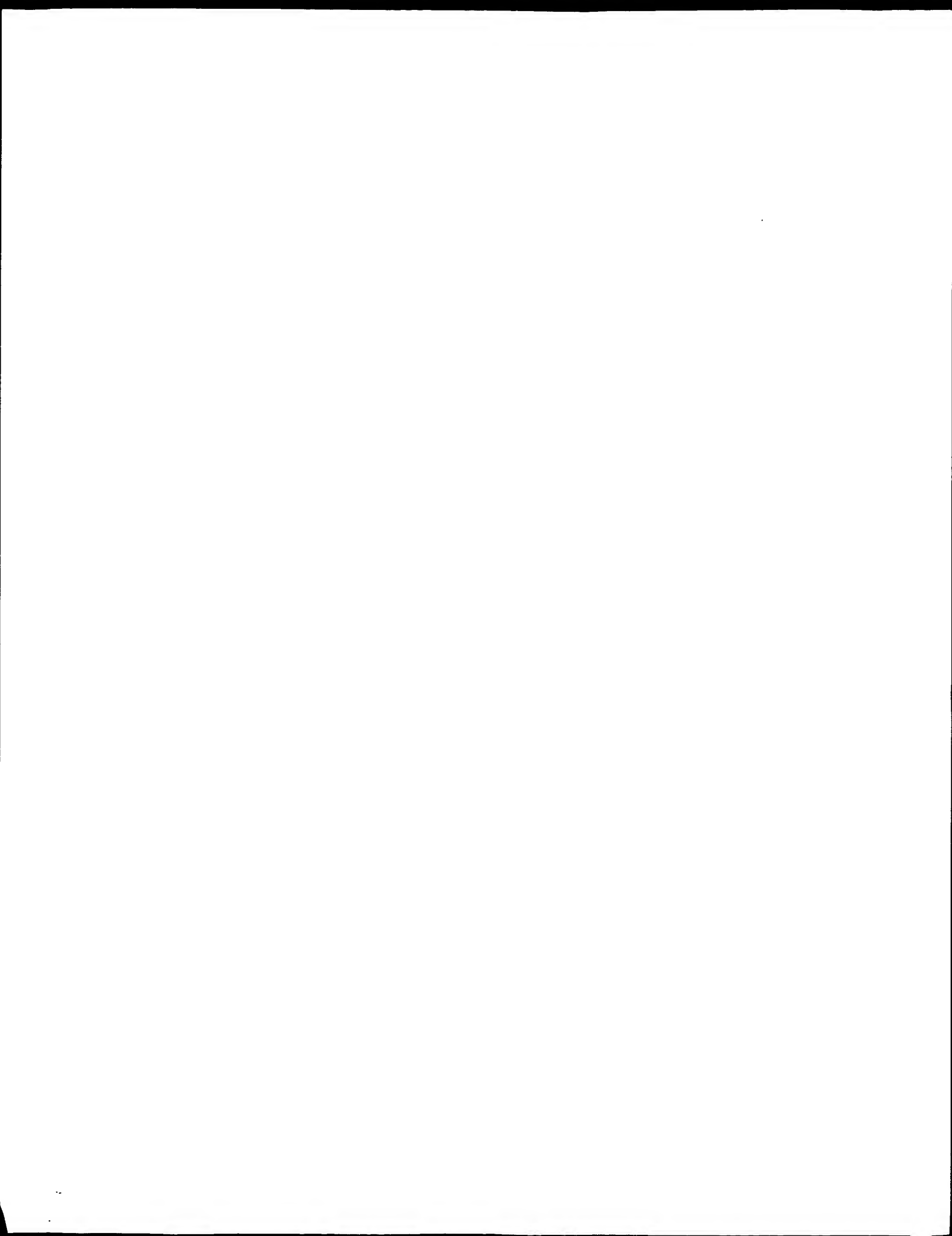
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DR N-PSDB; ABL92103.
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Claim 1; Page 206-207; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 23; Length 500;
 Best Local Similarity 100.0%; Pred. No. 1.4e-250;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPR 60
 DB 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPR 60
 QY 61 TOLSDQLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
 DB 61 TOLSDQLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
 QY 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 DB 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 181 NFNPGYSDNSTVYFDNGTVFVQWDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 QY 241 SYPETSSSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEVHRIELDFSKVTSMAVEFTP 300
 DB 241 SYPETSSSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEVHRIELDFSKVTSMAVEFTP 300
 QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGDFORYROEMWMDYGCQAQAEGRMCEDFQ 360
 DB 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGDFORYROEMWMDYGCQAQAEGRMCEDFQ 360
 QY 361 DEHDASAPDTSFSPYDGLTTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
 DB 361 DEHDASAPDTSFSPYDGLTTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
 QY 421 PVHLGTIVGLVAVLLVAAILLAGIYNGHPTSNALFFIERPHHWPAMKFRSHPDHST 480
 DB 421 PVHLGTIVGLVAVLLVAAILLAGIYNGHPTSNALFFIERPHHWPAMKFRSHPDHST 480
 QY 481 YAEVPEPSGHEKEGFMEAEQC 500
 DB 481 YAEVPEPSGHEKEGFMEAEQC 500

RESULT 2
 ID ABB90723
 XX ABB90723 standard; Protein; 1002 AA.
 AC ABB90723;
 XX
 DT 30-MAY-2002 (first entry)
 XX

DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
 XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX Homo sapiens.
 OS WO200210217-A2.
 PN 07-FEB-2002.
 PD 01-AUG-2001; 2001WO-US24031.
 PF 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX St Croix B, Kinzler KW, Vogelstein B;
 XX WPI; 2002-291856/33.
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Disclosure; Page 125-128; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 1002 AA;

Query Match 100.0%; Score 2691; DB 23; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 4e-250;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPR 60
 DB 503 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPR 562
 QY 61 TOLSDQLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
 DB 563 TOLSDQLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 622
 QY 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 DB 623 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 682
 QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 683 NFNPGYSDNSTVYFDNGTVFVQWDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
 QY 241 SYPETSSSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEVHRIELDFSKVTSMAVEFTP 300
 DB 743 SYPETSSSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEVHRIELDFSKVTSMAVEFTP 802
 QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGDFORYROEMWMDYGCQAQAEGRMCEDFQ 360

Db 803 LPTCLQHRSCDACWSSDLTFNCWCHVLRQCSGFDRIYRQWMDYGCQAEGRCDEDFQ 862
 Qy 361 DEDHDSAPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGSGDGLQNNLSPTKGT 420
 Db 863 DEDHDSAPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGSGDGLQNNLSPTKGT 922
 Qy 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFERRPHHPAMKFRSHPDHST 480
 Db 923 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFERRPHHPAMKFRSHPDHST 982
 Qy 481 YAEVPSGHEKEGFEAEQC 500
 Db 983 YAEVPSGHEKEGFEAEQC 1002
 RESULT 3
 ID ABB90729 standard; Protein: 500 AA.
 AC ABB90729;
 XX ABB90729;
 DT 30-MAY-2002 (first entry)
 DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
 XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX Mus musculus.
 OS WO200210217-A2.
 PN 07-FEB-2002.
 XX 01-AUG-2001; 2001WO-US24031.
 XX 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA St Croix B, Kinzler KW, Vogelstein B;
 PI WPI; 2002-291856/33.
 XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX Disclosure; Page 146-147; 331pp; English.
 PS The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX Sequence 500 AA;
 SQ

Query Match 82.1%; Score 2209; DB 23; Length 500;

Best Local Similarity 81.6%; Pred. No. 4.6e-204;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;
 Qy 1 MRGELWLL-VLVLREARALSPQAGHDEGPGSGWAAGKTGVRGNRRRARESPGHVSEPD 59
 Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEGQDSAWTAKTRQGWRRRPRESPAQLKPG 60
 Qy 60 RTOLSDILGGGTGLAMDTLPDNRTRVVEDNHSYVSLYGPSPHSELVDAEANRSOV 119
 Db 61 KTQLSDILGGGSGLAIDTLPDNRTRVVEDNHNHYVSVYGGKQSDLDVDAVANSHV 120
 Qy 120 KIHTILSNTHQASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179
 Db 121 KIHRLSSSHRQASRVVLSFDFPFYGHPLRQITATGGFIFMGDMLHRMLTATQYVAPLM 180
 Qy 180 ANENPGYSDNSTVYFDNGTIVVQNDHVVYLGWEDKSGSFTFOAALHHDGRIVFAYKEIP 239
 Db 181 ANENPGYSDNSTVAYFDNGTIVVQNDHVVYLDREDRGSFTFOAALHHDGRIVFAYKEIP 240
 Qy 240 MSVPEISSSOHPVKTGLSDAFMILNPNPDVPESSRRSIFEHRIELDPKSVTSMASVEFT 299
 Db 241 MAVLDISSAQHPVKAGLSDAFMILNNSPEVPSQRTIFEYHRVELDSKIITTSVAVET 300
 Qy 300 PLPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDRIYRQWMDYGCQAEGRCDECF 359
 Db 301 PLPTCLQHQCDTCVSNLTFNCWCHVLRQCSGFDRIYRQWMDYGCQAEGRCDECF 360
 Qy 360 QDEHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGSGDGLQNNLSPTKGT 419
 Db 361 QDHSYASPDSSFSFPGND-STTSSSLFIDSLTTEDDTKLNYPAGSGDGLDSSPSKSG 419
 Qy 420 TPVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFERRPHHPAMKFRSHPDHS 479
 Db 420 PPVHLGTIVGIVLAVLLVAAIILAGIYISGHPNSNAALFFERRPHHPAMKFRSHPDHS 479
 Qy 480 TYAEVPSGHEKEGFEAEQC 500
 Db 480 TYTEVPSGHEKEGFEAEQC 500
 RESULT 4
 ID ABB90783 standard; Protein: 500 AA.
 XX ABB90783;
 DT 30-MAY-2002 (first entry)
 DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.
 XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX Mus musculus.
 OS WO200210217-A2.
 PN 07-FEB-2002.
 XX 01-AUG-2001; 2001WO-US24031.
 XX 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA St Croix B, Kinzler KW, Vogelstein B;
 PI WPI; 2002-291856/33.
 XX

N-PSDB; ABL92136.

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -

Disclosure; Page 301-302; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumor growth, neoangiogenesis in subjects bearing a vascularised tumour; polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92073-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995.

Sequence 500 AA:

[illegible]

Db 295 TTSASPTSPFSDGDLTTSSSLFDLSLTEDDTKLNYPAGDGLQNNLSPKTKGTPVH 354

Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTNSAALFFIERRPHHPAMKFRSHDPDHTYAE 483

Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTNSAALFFIERRPHHPAMKFRSHDPDHTYAE 414

Qy 484 VEPGHEKEGFMEAEQC 500

Db 415 VEPGHEKEGFMEAEQC 431

RESULT 6

AAB43131

ID AAB43131 standard; Protein: 400 AA.

XX AC AAB43131;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.

DE Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerable; antipsoriatic; antiparkinsonian; neutropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

XX OS Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

XX N-PSDB; AAC77340.

XX Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 4955; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerable; antipsoriatic; antiparkinsonian; neutropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The

CC nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX SQ Sequence 400 AA;

Query Match 74.6%; Score 2007; DB 21; Length 400;

Best Local Similarity 100.0%; Pred. No. 1e-184;

Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 60

Db 29 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD 88

Qy 61 TQLSODLGGTTLAMDTPDNRTFVVEDNHSYVSRLYGPSEPHSRELWVDVAENRSQVK 120

Db 89 TQLSODLGGTTLAMDTPDNRTFVVEDNHSYVSRLYGPSEPHSRELWVDVAENRSQVK 148

Qy 121 IHTILSNTTHROASRVVLSDFPFYGHPLRQITTIATGCFIFMGDVIHRMLTATQYVAPLMA 180

Db 149 IHTILSNTTHROASRVVLSDFPFYGHPLRQITTIATGCFIFMGDVIHRMLTATQYVAPLMA 208

Qy 181 NENPGYSDNSTVYFNGVYVQVQWHDVYVQWEDKSGSTFOALHHDGRIVFAYKEIFM 240

Db 209 NENPGYSDNSTVYFNGVYVQVQWHDVYVQWEDKSGSTFOALHHDGRIVFAYKEIFM 268

Qy 241 SVPEISSQHPVKTGISDAFMIILNPDVPESRRRSIFEFVHRLELDPKSVTSMAVEFTP 300

Db 269 SVPEISSQHPVKTGISDAFMIILNPDVPESRRRSIFEFVHRLELDPKSVTSMAVEFTP 328

Qy 301 LPTCLQHRSCDACMSSDLTFNCISWCHVLRQCSGFDYRQEWMDYGCAGEGRMCEDFQ 360

Db 329 LPTCLQHRSCDACMSSDLTFNCISWCHVLRQCSGFDYRQEWMDYGCAGEGRMCEDFQ 388

Qy 361 DEHDSASPD 371

Db 389 DEHDSASPD 399

RESULT 7

AAB85396

ID AAB85396 standard; Protein: 499 AA.

XX AC AAB85396;

XX 17-SEP-2001 (first entry)

XX Stem cell growth factor-like polypeptide mature protein.

XX Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzheimer's disease; nutritional supplement; cytostatic; neutropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; cell proliferation; stem cell growth factor.

XX OS Homo sapiens.

XX WO200153500-A1.

XX 26-JUL-2001.

XX 23-DEC-2000; 2000WO-US35260.

XX 21-JAN-2000; 2000US-0488725.

XX 07-APR-2000; 2000US-0545714.

XX 11-APR-2000; 2000US-0547358.

Db 275 PVKVGSLDAFVVRHRIQIPNVRRTIYEHVRLVOMSKITNISAVEMTLPCTCLOFNRC 334

QY 311 DACMSSDLTFNCSWCHVLRQCSGDFRYRQWMDYGCQAEGRCMCEDFQDDHDSASPD 370

Db 335 GPCVSSQIGFNCWSCSKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTPEVETSSRTT 394

QY 371 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNPYAGGGLQ--NNLSPKTKGTPVHL 424

Db 395 TIGATTQFRVLTTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGTLHA 454

QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPKAMKFRSHPDHSTYAEV 484

Db 455 GLVIGLILVIVATALLVTVVYHPTSAASIFFIERRPSRWPAKPKRRSGHPPAYAEV 514

QY 485 EPSGHEKEGFMEEQ 500

Db 515 EPVG-EKEGFIIVSEQ 529

RESULT 9

ABB90726

ID ABB90726 standard; Protein: 529 AA.

XX AC ABB90726;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 189.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;

XX KW normal endothelial marker; pan-endothelial marker; immunostimulant;

XX KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;

XX KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;

XX KW psoriasis.

XX OS Homo sapiens.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US24031.

XX PR 02-AUG-2000; 2000US-222599P.

XX PR 11-AUG-2000; 2000US-224360P.

XX PR 11-APR-2001; 2001US-282850P.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX DR An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -

XX PS Disclosure; Page 140-141; 331pp; English.

XX CC The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences; tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995.

SQ Sequence 529 AA;

Query Match 48.1%; Score 1295; DB 23; Length 529;

Best Local Similarity 57.3%; Pred. No. 8.2e-116;

Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPNRRTRVVED-NHSYVSVRLXGCPSEPHSRLEWVDVAEANRQVQKIHTLSNTHR 130

Db 95 LLLDDGQDNNQIEEDTDHNYIISRYGPSDSASRDLLWVNDQMEKDKVKIHTLSNTHR 154

QY 131 QASRVVLSDFPFGHPLRQITATGFIEMGDVIHRLMTATQYVAPLMAFNFGYSDNS 190

Db 155 QAAVNLSDFEPFGHPLRQITATGFIEMGDVIHRLMTATQYVAPLMAFNFGYSDNS 214

QY 191 TVYFDNGTGVFVQNDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250

Db 215 TVRYFDNGTGVFVQNDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 274

QY 251 PVKGLSDAFVVRHRIQIPNVRRTIYEHVRLVOMSKITNISAVEMTLPCTCLOFNRC 310

Db 275 PVKGLSDAFVVRHRIQIPNVRRTIYEHVRLVOMSKITNISAVEMTLPCTCLOFNRC 334

QY 311 DACMSSDLTFNCSWCHVLRQCSGDFRYRQWMDYGCQAEGRCMCEDFQDDHDSASPD 370

Db 335 GPCVSSQIGFNCWSCSKLQRCSSGDFRHRQDWDVSGCPESKEKMCENTPEVETSSRTT 394

QY 371 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNPYAGGGLQ--NNLSPKTKGTPVHL 424

Db 395 TIGATTQFRVLTTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGTLHA 454

QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPKAMKFRSHPDHSTYAEV 484

Db 455 GLVIGLILVIVATALLVTVVYHPTSAASIFFIERRPSRWPAKPKRRSGHPPAYAEV 514

QY 485 EPSGHEKEGFMEEQ 500

Db 515 EPVG-EKEGFIIVSEQ 529

RESULT 10

ABB90734

ID ABB90734 standard; Protein: 529 AA.

XX AC ABB90734;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 200.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;

XX KW normal endothelial marker; pan-endothelial marker; immunostimulant;

XX KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;

XX KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;

XX KW psoriasis.

XX OS Homo sapiens.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US24031.

XX PR 02-AUG-2000; 2000US-222599P.

XX PR 11-AUG-2000; 2000US-224360P.

XX PR 11-APR-2001; 2001US-282850P.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX DR N-PSDB; ABL92088.

QY 485 EPSCKEKEGMEAEQC 500
 Db 515 EPVG-EKEGFIVSEQ 529

RESULT 13
 AAB31211

ID AAB31211 standard; Protein; 529 AA.
 XX AAB31211;
 AC AAB31211;
 XX 20-APR-2001 (first entry)
 XX Amino acid sequence of human polypeptide PRO6003.
 DE Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
 KW PRO183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
 KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
 KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 42..48
 FT /note= "N-myristoylation site"
 FT Modified-site 100..106
 FT /note= "N-myristoylation site"
 FT Modified-site 103..107
 FT /note= "N-glycosylation site"
 FT Modified-site 147..153
 FT /note= "N-myristoylation site"
 FT Modified-site 160..164
 FT /note= "N-glycosylation site"
 FT Modified-site 213..217
 FT /note= "N-glycosylation site"
 FT Modified-site 221..225
 FT /note= "N-glycosylation site"
 FT Modified-site 279..285
 FT /note= "N-myristoylation site"
 FT Modified-site 297..301
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 316..320
 FT /note= "N-glycosylation site"
 FT Modified-site 345..349
 FT /note= "N-glycosylation site"
 FT Modified-site 397..403
 FT /note= "N-myristoylation site"
 FT Modified-site 450..456
 FT /note= "N-myristoylation site"
 FT Domain 454..478
 FT /note= "transmembrane domain"
 FT Modified-site 455..461
 FT /note= "N-myristoylation site"
 FT Modified-site 492..496
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 503..507
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 PN W0200077037-A2.
 XX 21-DEC-2000.
 XX 22-MAY-2000; 2000WO-US14042.
 XX 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.

01-SEP-1999; 99WO-US20111.
 08-SEP-1999; 99WO-US20594.
 15-SEP-1999; 99WO-US21090.
 15-SEP-1999; 99WO-US21547.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28301.
 02-DEC-1999; 99US-US28565.
 07-DEC-1999; 99US-0169495.
 05-JAN-2000; 2000WO-US00219.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 22-FEB-2000; 2000WO-US04414.
 01-MAR-2000; 2000WO-US05601.
 02-MAR-2000; 2000WO-US05841.
 20-MAR-2000; 2000WO-US07377.
 30-MAR-2000; 2000WO-US08439.
 15-MAY-2000; 2000WO-US13358.
 17-MAY-2000; 2000WO-US13705.
 (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 DR WPI: 2001-050091/06.
 N-PSDB; AAB31211.
 XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides -
 XX
 PS Claim 12; Fig 66; 244pp; English.
 XX The present sequence represents a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO1361, PRO1308, PRO183, PRO1272, PRO1419, PRO4999, PRO7170,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO333, PRO301, PRO187,
 CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of calls
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding of these
 CC polypeptides are useful in the recombinant production of the
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene.
 XX Sequence 529 AA;
 SQ
 Query Match 48.1%; Score 1294; DB 22; Length 529;
 Best Local Similarity 57.1%; Pred. No. 1e-115;
 Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;
 QY 72 LAMDTLPDNRTRVVED-NH5YVSRLYGSPSPHRELWVDVAEANRQVKTHITLSNTHR 130
 Db LLLDDGQDNNTQIEDTHNYIISRIYGPSDSASRDMLWNIDQMKDKVTHGLSNTHR 154
 QY 131 QASRVLSDFPFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMANFNFGSDNS 190
 Db QAAARNVLSDFPFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMANFNFGSDNS 214
 QY 191 TVVYDNGTVEVQVDHVLQGWEDKGSFTFOAALHHDGRIVFAKKEIPMSVPEISSQH 250
 Db TVRFDNGTALVQVDHVLQGWEDKGSFTFOAALHHDGRIVFAKKEIPMSVPEISSQH 274
 QY 251 PVKTGLSDAFMILNPSDPVPSRRRSIFEVHRIELDFSKVTSMSAVEFTPLPTCLQHRSC 310
 Db PVKTGLSDAFMILNPSDPVPSRRRSIFEVHRIELDFSKVTSMSAVEFTPLPTCLQHRSC 310

PT Isolated polypeptide with stem cell growth factor-like activity for
PT treatment of leukemia, hemophilia, and degenerative diseases like
PT Alzheimer's disease and to generate new tissues and organs -
XX
XX
XX Claim 10; Page 147-149; 154pp; English.
XX
XX The invention provides novel human stem cell growth factor-like
XX polypeptides and polynucleotides encoding them. The polypeptides having
XX stem cell growth factor-like activity, can be expressed by standard
XX recombinant methodology. The polynucleotides and polypeptides can be
XX used to induce differentiation of embryonic and adult stem cells to give
XX rise to different cell types. They may also be used in the treatment of
XX leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
XX They may also be utilized to generate new tissues and organs that may aid
XX patients in need of transplants. They can also be used as nutritional
XX supplements. The present sequence represents a stem cell growth factor-
XX like polypeptide fragment.

SQ Sequence 425 AA;

Query Match 47.4%; Score 1276; DB 22; Length 425;
Best Local Similarity 57.7%; Pred. NO. 4e-114;
Matches 248; Conservative 64; Mismatches 106; Indels 12; Gaps 5;
QY 78 PDNRTRVVEDNHSYVSRLYGSEPHSRELWVDVAENRQVKIHTILSNTHROASRVVL 137
Db 1 PRVPRVRTD-HNYIYSRIYGPDSASRDLWNIDOMEKDKYKIGILSNTHROAARVNL 59
QY 138 SFDFPFYGHPLROITATGGIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVWYFDN 197
Db 60 SFDFPFYGHFLREITVATGGIYTGVEVHRMLTATQYIAPLMANFDPVSRSNSTVRYFDN 119
QY 198 GTVFWQNDHYVLOQWEDKSGFTQAAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257
Db 120 GTALVVQNDHVHLQDNYNLGSFTQATLLMDGRIFGFIQVPLVLTQISSTNHPKVGLS 179
QY 258 DAFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTPLPTCLOHRS CDACMSD 317
Db 180 DAFVVVHRIQIPNVRRITIEYHRVQLQMSKIINISAVEMTLPCLQNRGCPVSSQ 239
QY 318 LTFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCED-----FQDEDHDSASPD 371
Db 240 IGFCNCSKLRGSSGFDHRQDWDVDSGCPESKEKMCNTEPVTFLPPQPERQPPS 299
QY 372 SFSPYDGLTTSSLSLFTDSTEDDTKLNPYAGDGLQ-NLSPKTKTPVHLGTIVGI 430
Db 300 SGLPPEDAVT---SQFTSLPTEDDTKIALHLKDNAGASTDDSAEEKGGTLHAGLIVGI 356
QY 431 VLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEVPSGHE 490
Db 357 LILVLIVATAILVTVMYVHHPTSAASIFFIERRPSRPAMKFRGSGHPAYAEVPGV-E 415
QY 491 KEGFWEAEOC 500
Db 416 KEGFIVSEQ 425

Search completed: April 22, 2003, 16:06:33
Job time : 81 secs

PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234397.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX N-PSDB; AAK61650.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX Claim 11; SEQ ID NO 16462; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 205 AA;
Query Match 21.6%; Score 108; DB 22; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-100;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 236 KEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYRIELDPKSVTMSA 295
Db 58 KEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYRIELDPKSVTMSA 117
QY 296 VEFTPLPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEW 343
Db 118 VEFTPLPTCLOHRSCDACMSSDLTFNCWCHVLQRCSSGFDYRQEW 165
RESULT 7
AAW58986
ID AAW58986 standard; Protein; 108 AA.
XX
AC AAW58986;
XX
DT 11-SEP-1998 (first entry)
XX Homo sapiens adult brain clone CC194_4 encoded protein.
DE Homo sapiens adult brain clone CC194_4; secreted protein
XX adult; brain; cDNA library; clone CC194_4; secreted protein
KW autoimmune disease; anti-inflammatory; immune; stimulation
KW suppression.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 40 /note= "undefined amino acid, encoded by AMT"
PR

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
OS Homo sapiens.
XX WO200190304-A2.
XX 29-NOV-2001.
XX 18-MAY-2001; 2001WO-US16450.
XX 19-MAY-2000; 2000US-205515P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
XX WPI; 2002-122018/16.
XX N-PSDB; ABL90486.
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX Claim 11; SEQ ID NO 2453; 2081pp + Sequence Listing; English.
XX The invention relates to novel genes (ABL9449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 146 AA;
Query Match 26.0%; Score 130; DB 23; Length 146;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 343 MDYCAQAEAGRMCEDEQDEHDSASDPTSFSPYDGLTTTSSSLFIDSITDDTKLNP 402
Db 1 MDYCAQAEAGRMCEDEQDEHDSASDPTSFSPYDGLTTTSSSLFIDSITDDTKLNP 60
QY 403 YAGDGLQNNLSPKTKGTPVHLGTVIGVILVALLVAAILAGIYINGHPTSNALFFIER 462
Db 61 YAGDGLQNNLSPKTKGTPVHLGTVIGVILVALLVAAILAGIYINGHPTSNALFFIER 120
QY 463 RPHWPAKMF 472
Db 121 RPHWPAKMF 130
RESULT 6
AA88869
ID AA88869 standard; Protein: 205 AA.
XX

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus, lupus
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 400 AA;

Query Match 74.2%; Score 371; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELMLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRRARESGPHVSEPR 60
 DB 29 MRGELMLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRRARESGPHVSEPR 88
 QY 61 TQLSDQLGGTAMDPLPNRRTRVEDNHSYVSRLYGSPHSELWVDVAENRSQVK 120
 DB 89 TQLSDQLGGTAMDPLPNRRTRVEDNHSYVSRLYGSPHSELWVDVAENRSQVK 148
 QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
 DB 149 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 208
 QY 181 NFNPYSDNSTVYFNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 209 NFNPYSDNSTVYFNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 268
 QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
 DB 269 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 328
 QY 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGGFDYRQEWMDYGCAGEGRMCEDFQ 360
 DB 329 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGGFDYRQEWMDYGCAGEGRMCEDFQ 388
 QY 361 DEHDHSASPT 371
 DB 389 DEHDHSASPT 399

RESULT 4
 AAB85400
 ID AAB85400 standard; Protein; 431 AA.
 XX
 AC AAB85400;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Tumour endothelial marker 7 precursor protein.
 XX
 KW Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
 KW degenerative disease; Alzheimer's disease; nutritional supplement;
 KW cytostatic; neurotropic; neuroprotective; hemostatic; antisense-therapy;
 KW gene-therapy; tumour endothelial marker 7 precursor protein.
 XX
 OS Homo sapiens.

XX WO200153500-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 23-DEC-2000; 2000WO-US35260.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 07-APR-2000; 2000US-0545714.
 PR 11-APR-2000; 2000US-0547358.
 XX (HYSE-) HYSEQ INC.
 PA Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;
 PI Chao C;
 PI WPI: 2001-451909/48.
 DR
 XX Isolated polypeptide with stem cell growth factor-like activity for
 PT treatment of leukemia, hemophilia, and degenerative diseases like
 PT Alzheimer's disease and to generate new tissues and organs -
 XX
 PS Example 4; Page 149-150; 154pp; English.
 XX
 CC The invention provides novel human stem cell growth factor-like
 CC polypeptides and polynucleotides encoding them. The polypeptides having
 CC stem cell growth factor-like activity, can be expressed by standard
 CC recombinant methodology. The polynucleotides and polypeptides can be
 CC used to induce differentiation of embryonic and adult stem cells to give
 CC rise to different cell types. They may also be used in the treatment of
 CC leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
 CC They may also be utilized to generate new tissues and organs that may aid
 CC patients in need of transplants. They can also be used as nutritional
 CC supplements. The present sequence represents a tumour endothelial marker
 CC 7 precursor protein, homologous to a stem cell growth factor-like
 CC polypeptide.
 XX
 SQ Sequence 431-AA;

Query Match 54.2%; Score 271; DB 22; Length 431;
 Best Local Similarity 100.0%; Pred. No. 5.3e-264;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LAMDTLPDNRTRVEDNHSYVSRLYGSPHSELWVDVAENRSQVKIHTILSNTHRQ 131
 DB 1 LAMDTLPDNRTRVEDNHSYVSRLYGSPHSELWVDVAENRSQVKIHTILSNTHRQ 60
 QY 132 ASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAENFPGYSDNST 191
 DB 61 ASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAENFPGYSDNST 120
 QY 192 VVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 251
 DB 121 VVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180
 QY 252 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPTCLQHRSCD 311
 DB 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPTCLQHRSCD 240
 QY 312 ACMSSDLTFNCWCHVLRQCSGGFDYRQEW 342
 DB 241 ACMSSDLTFNCWCHVLRQCSGGFDYRQEW 271

RESULT 5
 ABB90077
 ID ABB90077 standard; Protein; 146 AA.
 XX
 AC ABB90077;
 XX 24-MAY-2002 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 2453.

ID XX ABB90723 standard; Protein; 1002 AA.
AC ABB90723;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX
OS Homo sapiens.
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US24031.
XX
PR 02-AUG-2000; 2000US-222599P.
PR 11-AUG-2000; 2000US-224360P.
PR 11-APR-2001; 2001US-282850P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2002-291856/33.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth -
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PS Disclosure; Page 125-128; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in
CC subjects bearing a vascularised tumour, polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX
SQ Sequence 1002 AA;
Query Match 100.0%; Score 500; DB 23; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSPDR 60
DB 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSEPD 562
QY 61 TOLSDGLGGTTLAMDTPDNTRVVEDNHSYVSRLYGPPSPHRELWVDVAENRSQVK 120
DB 563 TOLSDGLGGTTLAMDTPDNTRVVEDNHSYVSRLYGPPSPHRELWVDVAENRSQVK 622
QY 121 IHTILSNTHRAQSRVLSFDPFPGHPLRQITATGTFIEMGDVTHRMLTATQYVAPLMA 180
DB 623 IHTILSNTHRAQSRVLSFDPFPGHPLRQITATGTFIEMGDVTHRMLTATQYVAPLMA 682
QY 101 NFNPGYSDNSTVYFDNGTVEVQWQHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVYFDNGTVEVQWQHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742

QY 241 SVPELSSQHPVKTKLSDAFMILNPSDPVPSRRRSIFEXHRIELDFSKVTSMAVEFTP 300
DB 743 SVPELSSQHPVKTKLSDAFMILNPSDPVPSRRRSIFEXHRIELDFSKVTSMAVEFTP 802
QY 301 LPTCLQHRSCDACMSSDLTFNCMSCHVLCORSSGDFRYROEMWDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSSDLTFNCMSCHVLCORSSGDFRYROEMWDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 863 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 922
QY 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAIFFERRPHHPAMPKFRSHPDHST 480
DB 923 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAIFFERRPHHPAMPKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMPEAQC 500
DB 983 YAEVPSGHEKEGFMPEAQC 1002
RESULT 3
AAB43131
ID AAB43131 standard; Protein; 400 AA.
XX
AC AAB43131;
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DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.
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OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
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PF 31-MAR-2000; 2000WO-US08621.
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PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
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PI Shimketa RA, Leach M;
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DR WPI: 2000-602362/57.
DR N-PSDB; AAC77340.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
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PS Claim 11; Page 4955; 5507pp; English.
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814	1.2	193	22	AAM15133	Peptide #1567 enco	887	6	1.2	214	22	AAG90925	C glutamicum prote
815	1.2	193	22	AAM27588	Peptide #1625 enco	888	6	1.2	214	23	ABB77890	Amino acid sequenc
816	1.2	193	22	AAM02874	Peptide #1556 enco	889	6	1.2	215	21	AAB54208	Human pancreatic c
817	1.2	193	23	ARG36943	Human peptide enco	890	6	1.2	215	21	AAG04896	Arabidopsis thalia
818	1.2	193	23	ABB47646	Listeria monocytog	891	6	1.2	215	21	AAG50849	Arabidopsis thalia
819	1.2	194	20	AA373221	Amino acid sequenc	892	6	1.2	215	22	AAG66289	Human tankyrase2 c
820	1.2	194	21	AAG07582	Arabidopsis thalia	893	6	1.2	215	23	ABB77893	Amino acid sequenc
821	1.2	195	21	AAG07313	Arabidopsis thalia	894	6	1.2	216	21	AAG51946	Arabidopsis thalia
822	1.2	195	22	ABH80090	Corynebacterium gl	895	6	1.2	216	23	ABP29667	Human polyptide
823	1.2	195	22	ABH41856	Human ovarian anti	896	6	1.2	216	23	ABB89202	Arabidopsis thalia
824	1.2	195	23	ABB06799	Human nPCR-Seql01	897	6	1.2	217	21	AAG17021	Arabidopsis thalia
825	1.2	196	18	AAM26746	S. carnosus nitrat	898	6	1.2	218	22	ABB66933	Drosophila melanog
826	1.2	196	21	AAG17022	Arabidopsis thalia	899	6	1.2	218	22	AAG69760	Escherichia coli U
827	1.2	196	21	AAG51947	Arabidopsis thalia	900	6	1.2	218	23	AAU11282	Human testicular t
828	1.2	196	22	AAU29434	Human G protein-co	901	6	1.2	219	22	ABP66771	Drosophila melanog
829	1.2	196	23	ABG60722	Novel G protein-co	902	6	1.2	219	23	AAU92997	Arabidopsis transc
830	1.2	197	23	ABG29524	Streptococcus poly	903	6	1.2	220	22	ABH68171	Drosophila melanog
831	1.2	197	23	AAE18281	Bovine fertility a	904	6	1.2	220	22	AAU42147	Propionibacterium
832	1.2	197	23	AAE18281	Bovine fertility a	905	6	1.2	221	22	ABG23687	Novel human diagno
833	1.2	198	21	AAB411516	Bovine fertility-a	906	6	1.2	221	22	ABG23687	C glutamicum prote
834	1.2	198	22	ABB31735	Human ORFX ORF2118	907	6	1.2	221	23	ABP41862	Human ovarian anti
835	1.2	198	22	ABB36957	Peptide #4386 enco	908	6	1.2	221	23	ABP40139	Staphylococcus epi
836	1.2	198	22	ABB22271	Peptide #4463 enco	909	6	1.2	222	12	ABP27808	Streptococcus poly
837	1.2	198	22	AAU25706	Protein #4270 enco	910	6	1.2	222	12	AAR13943	Calcium channel ga
838	1.2	198	22	AAU25706	G protein-coupled	911	6	1.2	222	20	AAW78210	Human secreted pro
839	1.2	198	22	AAU57690	Human brain expres	912	6	1.2	222	21	AAU54894	Human secreted pro
840	1.2	198	22	AAU70097	Human bone marrow	913	6	1.2	222	22	AAU45233	Arabidopsis thalia
841	1.2	198	22	AAU17924	Peptide #4358 enco	914	6	1.2	222	22	ABG27005	Propionibacterium
842	1.2	198	22	AAU30436	Peptide #4473 enco	915	6	1.2	222	22	AAU73292	Novel human diagno
843	1.2	198	22	AAU55574	Peptide #4256 enco	916	6	1.2	222	23	AAU75170	Murine TSG-like pr
844	1.2	198	23	ABG39732	Human peptide enco	917	6	1.2	223	18	AAW32112	Mouse BMP polypept
845	1.2	199	18	AAW34131	Streptococcus pneu	918	6	1.2	223	19	AAW70591	A novel human cyto
846	1.2	199	18	AAW37151	Dirofilaria immiti	919	6	1.2	223	20	AAU28504	Human growth facto
847	1.2	199	19	AAW71493	Helicobacter polyp	920	6	1.2	223	20	ABH67311	HGFH4 Human Growth
848	1.2	199	22	AAU92802	S. pneumoniae hist	921	6	1.2	223	22	AAH88460	Drosophila melanog
849	1.2	199	22	ABP46314	H. pylori HPC134 p	922	6	1.2	223	22	AAH88460	Human membrane or
850	1.2	199	23	ABP38980	Staphylococcus epi	923	6	1.2	223	23	ABP42145	Human D-SLAM extra
851	1.2	200	19	AAU11076	Listeria monocytog	924	6	1.2	223	23	ABP42145	Human ovarian anti
852	1.2	200	20	AAU11076	H. pylori ORF hp4e	925	6	1.2	224	21	ABH41233	Listeria monocytog
853	1.2	200	20	AAU11076	S. epidermidis ope	926	6	1.2	224	22	ABG12473	Human ORFX ORF997
854	1.2	201	21	AAU11076	S. epidermidis ope	927	6	1.2	224	22	ABG12473	Novel human diagno
855	1.2	201	21	AAU11076	Arabidopsis thalia	928	6	1.2	226	21	AAH18451	Human novel secret
856	1.2	201	21	AAU11076	Arabidopsis thalia	929	6	1.2	226	21	AAH18451	Human ORFX ORF3031
857	1.2	201	22	AAU11076	Human tonka protel	930	6	1.2	226	21	AAH18451	A human TANGO 262
858	1.2	201	22	AAU11076	Novel human diagno	931	6	1.2	226	21	AAH18451	A human TANGO 262
859	1.2	201	23	AAU11076	Human fertility-as	932	6	1.2	226	21	AAH18451	A human TANGO 262
860	1.2	202	21	AAU11076	Fragment of human	933	6	1.2	226	21	AAH18451	A murine TANGO 262
861	1.2	202	21	AAU11076	Neisseria gonorrhoe	934	6	1.2	226	21	AAH18451	A murine TANGO 262
862	1.2	202	21	AAU11076	Novel human diagno	935	6	1.2	226	21	AAH18451	A murine TANGO 262
863	1.2	202	21	AAU11076	Human EST encoded	936	6	1.2	226	21	AAH18451	A murine TANGO 262
864	1.2	202	21	AAU11076	Staphylococcus epi	937	6	1.2	226	21	AAH18451	Human secreted pro
865	1.2	202	21	AAU11076	Propionibacterium	938	6	1.2	226	21	AAH18451	Human secreted pro
866	1.2	202	21	AAU11076	Propionibacterium	939	6	1.2	226	21	AAH18451	Drosophila melanog
867	1.2	202	21	AAU11076	H. pylori ORF 05cp	940	6	1.2	226	22	AAU29084	Human PRO polypt
868	1.2	202	21	AAU11076	dTDP-4-keto-6-deox	941	6	1.2	226	22	AAU29084	S. avermitilis ORF
869	1.2	202	21	AAU11076	Arabidopsis thalia	942	6	1.2	226	22	AAU29084	Human PRO1079 (UNQ
870	1.2	202	21	AAU11076	Arabidopsis thalia	943	6	1.2	226	22	AAU29084	Secreted protein #
871	1.2	202	21	AAU11076	C glutamicum prote	944	6	1.2	226	22	AAU29084	Human secreted pro
872	1.2	202	21	AAU11076	Human tankyrase2 c	945	6	1.2	226	22	AAU29084	Human angiogenesis
873	1.2	202	21	AAU11076	Streptococcus pneu	946	6	1.2	226	23	AAU29084	Human PRO1079 prot
874	1.2	202	21	AAU11076	Human secreted pro	947	6	1.2	227	22	AAU29084	Human secreted pro
875	1.2	202	21	AAU11076	S. epidermidis ope	948	6	1.2	227	22	AAU29084	Novel human diagno
876	1.2	202	21	AAU11076	S. epidermidis ope	949	6	1.2	227	22	AAU29084	Streptococcus poly
877	1.2	202	21	AAU11076	Drosophila melanog	950	6	1.2	228	21	AAU29084	Arabidopsis thalia
878	1.2	202	21	AAU11076	Novel human diagno	951	6	1.2	228	21	AAU29084	Arabidopsis thalia
879	1.2	202	21	AAU11076	Mouse osteoblast d	952	6	1.2	228	22	AAU29084	Mouse surface glyco
880	1.2	202	21	AAU11076	Arabidopsis thalia	953	6	1.2	229	11	AAU29084	Murine protein iso
881	1.2	202	21	AAU11076	Arabidopsis thalia	954	6	1.2	229	22	AAU29084	Preprolactin from
882	1.2	202	21	AAU11076	Streptococcus poly	955	6	1.2	229	23	AAU29084	Novel human secret
883	1.2	202	21	AAU11076	Streptococcus poly	956	6	1.2	230	22	AAU29084	Novel secreted pro
884	1.2	202	21	AAU11076	Pheromone receptor	957	6	1.2	232	21	AAU29084	Propionibacterium
885	1.2	202	21	AAU11076	Arabidopsis thalia	958	6	1.2	232	21	AAU29084	Arabidopsis thalia
886	1.2	202	21	AAU11076	Human polyptide	959	6	1.2	232	21	AAU29084	Arabidopsis thalia
					Drosophila melanog							

668	6	1.2	146	22	AAU56080	Propionibacterium	741	6	1.2	167	21	AAG14830	Arabidopsis thalia
669	6	1.2	147	22	AAU22335	Human cardiovascular	742	6	1.2	167	22	AAU48946	Propionibacterium
670	6	1.2	148	23	ABB53904	Lactococcus lactis	743	6	1.2	168	23	ABP89999	Human polypeptide
671	6	1.2	149	23	ABB55165	Lactococcus lactis	744	6	1.2	170	21	AGL14829	Arabidopsis thalia
672	6	1.2	148	13	AAR36410	Human phospholipase	745	6	1.2	170	22	AAU41312	Propionibacterium
673	6	1.2	148	16	AAR36410	Human phospholipase	746	6	1.2	170	22	AAU23046	Novel human enzyme
674	6	1.2	148	22	AAB94451	Human protein sequ	747	6	1.2	170	22	AGG30397	C glutamic prote
675	6	1.2	148	23	AAB78667	Human phospholipase	748	6	1.2	170	23	ABP90048	Human polypeptide
676	6	1.2	148	23	AAU78668	Human phospholipase	749	6	1.2	172	21	AGL12942	Arabidopsis thalia
677	6	1.2	149	22	AAU78668	Human phospholipase	750	6	1.2	172	21	AGG36892	Arabidopsis thalia
678	6	1.2	150	20	AAU36774	Human immune/haema	751	6	1.2	172	22	AAU13544	Human polypeptide
679	6	1.2	150	21	AAU10880	Chlamydia trachoma	752	6	1.2	172	23	ABP42854	Human ovarian anti
680	6	1.2	150	22	ABG10880	Arabidopsis thalia	753	6	1.2	172	23	ABP43436	Human OREX protein
681	6	1.2	151	22	ABG11453	Drosophila melanog	754	6	1.2	172	23	ABP04807	Human OREX protein
682	6	1.2	151	22	AAU32409	Novel human secret	755	6	1.2	173	21	AGL15810	Arabidopsis thalia
683	6	1.2	151	23	ABP53870	Lactococcus lactis	756	6	1.2	173	23	ABP29065	Streptococcus poly
684	6	1.2	152	22	AAU23400	Novel human enzyme	757	6	1.2	174	19	ABP20786	Human neurofilamen
685	6	1.2	153	10	AAU90380	Sequence of sorbin	758	6	1.2	174	22	AAU71930	Human bone marrow
686	6	1.2	153	22	AAU47278	Propionibacterium	759	6	1.2	175	21	ABG32725	Eucalyptus grandis
687	6	1.2	153	22	ABG01976	Novel human diagno	760	6	1.2	175	21	AGG04897	Arabidopsis thalia
688	6	1.2	153	22	AAE13103	Human phospholipase	761	6	1.2	175	21	AGG050850	Arabidopsis thalia
689	6	1.2	153	22	AAE13103	Amino acid sequenc	762	6	1.2	175	23	ABP81489	Mouse zifnrl2 prot
690	6	1.2	153	23	ABP33830	Human transport pr	763	6	1.2	175	23	ABP22244	Murine BAPF recept
691	6	1.2	154	20	AAU81994	Tobacco trehalase	764	6	1.2	175	23	ABP22244	Human polypeptide
692	6	1.2	155	22	AAU50821	Propionibacterium	765	6	1.2	176	21	ABP32819	Eucalyptus grandis
693	6	1.2	155	22	AAU50821	C glutamic prote	766	6	1.2	176	21	AAU74637	Neisseria meningit
694	6	1.2	156	21	AAU50821	Human pancreatic c	767	6	1.2	176	21	AAU74637	Neisseria meningit
695	6	1.2	156	21	AAU50821	Arabidopsis thalia	768	6	1.2	176	21	AAU74637	Human polypeptide
696	6	1.2	156	22	AAU50821	Rat EST encoded pr	769	6	1.2	177	23	ABP90213	Amino acid sequenc
697	6	1.2	156	23	ABP25729	Streptococcus poly	770	6	1.2	178	20	ABP37942	Novel human diagno
698	6	1.2	157	21	ABP16353	Eucalyptus grandis	771	6	1.2	178	22	ABG09621	Novel human diagno
699	6	1.2	157	21	AAU18510	Zea mays protein f	772	6	1.2	179	21	AGL10879	Arabidopsis thalia
700	6	1.2	157	22	AAU06736	Human polypeptide	773	6	1.2	179	22	ABP67684	Drosophila melanog
701	6	1.2	157	22	AAU06736	Human olfactory re	774	6	1.2	179	22	ABP67684	Drosophila melanog
702	6	1.2	158	21	AAU06736	Human tankyrase2 c	775	6	1.2	180	21	AGL11936	Arabidopsis thalia
703	6	1.2	158	21	AAU06736	Arabidopsis thalia	776	6	1.2	181	22	ABG14207	Novel human diagno
704	6	1.2	158	22	AAU06736	Amino acid sequenc	777	6	1.2	181	22	ABP30701	Human expressed po
705	6	1.2	158	22	AAU06736	Bovine mammary tis	778	6	1.2	181	22	ABP30701	Novel human enzyme
706	6	1.2	158	22	AAU06736	Corynebacterium gl	779	6	1.2	181	23	AAE22126	Human 54372 domain
707	6	1.2	159	21	AAU06736	Arabidopsis thalia	780	6	1.2	182	21	AGG07583	Arabidopsis thalia
708	6	1.2	159	21	AAU06736	Arabidopsis thalia	781	6	1.2	182	22	AGG01010	Novel human diagno
709	6	1.2	159	21	AAU06736	Arabidopsis thalia	782	6	1.2	183	21	AGG07315	Arabidopsis thalia
710	6	1.2	159	21	AAU06736	Zea mays protein f	783	6	1.2	183	22	ABP63065	Drosophila melanog
711	6	1.2	159	21	AAU06736	Zea mays protein f	784	6	1.2	184	20	ABP35695	Chlamydia pneumoni
712	6	1.2	159	22	AAU06736	Streptococcus pneu	785	6	1.2	184	22	AAU66191	Zea mays protein f
713	6	1.2	159	22	AAU06736	Novel human secret	786	6	1.2	184	22	AAU66191	Propionibacterium
714	6	1.2	160	23	ABP80777	A. salmonicida typ	787	6	1.2	184	23	AAU49392	Human ATP-depend
715	6	1.2	160	23	AAE20506	Streptococcus muta	788	6	1.2	185	21	AGG43191	Arabidopsis thalia
716	6	1.2	161	20	AAU38038	Streptococcus muta	789	6	1.2	185	21	AGG43191	Arabidopsis thalia
717	6	1.2	161	20	AAU38038	Neisseria meningit	790	6	1.2	185	22	ABP63787	Drosophila melanog
718	6	1.2	161	20	AAU38038	Neisseria gonorrhoe	791	6	1.2	185	22	AAU67318	Propionibacterium
719	6	1.2	161	21	AAU38038	Zea mays protein f	792	6	1.2	185	22	AAU67318	Human gastric can
720	6	1.2	162	22	ABG11474	Novel human diagno	793	6	1.2	185	22	AAU67318	Z. mays COII. Zea
721	6	1.2	162	22	ABG44098	Peptide #11604 enc	794	6	1.2	186	21	AAU01926	Corn COII protein
722	6	1.2	162	22	ABP26988	Protein #8987 enco	795	6	1.2	186	21	AAU23455	Human polypeptide
723	6	1.2	162	22	ABP26988	Human expressed po	796	6	1.2	186	22	AAU43545	Human novel foetal
724	6	1.2	162	22	AAU7827	Human brain expres	797	6	1.2	187	22	AAU21166	Arabidopsis thalia
725	6	1.2	162	22	AAU7827	Human bone marrow	798	6	1.2	188	21	AGG07314	Arabidopsis thalia
726	6	1.2	162	22	AAU7827	Human immune/haema	799	6	1.2	188	21	AGG07314	Arabidopsis thalia
727	6	1.2	162	22	AAU7827	Peptide #8164 enco	800	6	1.2	189	21	AGG36797	Arabidopsis thalia
728	6	1.2	162	22	AAU7827	Peptide #12083 enc	801	6	1.2	189	22	AAU46243	Propionibacterium
729	6	1.2	162	23	ABG46858	Callitrix jacchus	802	6	1.2	189	22	AAU46243	Arabidopsis thalia
730	6	1.2	163	22	AAE12071	Human peptide enco	803	6	1.2	190	21	AGG3190	Human G protein-co
731	6	1.2	163	22	AAE12071	Dendritic cell (DC	804	6	1.2	191	22	AAU29508	Novel human secret
732	6	1.2	164	20	AAU27204	Amino acid sequenc	805	6	1.2	191	22	AAU31296	Novel G protein co
733	6	1.2	164	21	AAU27204	Human secreted pro	806	6	1.2	191	22	ABG60796	Drosophila melanog
734	6	1.2	164	21	AAU27204	Arabidopsis thalia	807	6	1.2	192	22	ABG66695	Arabidopsis thalia
735	6	1.2	164	21	AAU27204	Arabidopsis thalia	808	6	1.2	193	21	AGG4795	Peptide #1608 enco
736	6	1.2	164	22	AAU66663	Membrane-bound pro	809	6	1.2	193	22	ABP28957	Peptide #1631 enco
737	6	1.2	164	22	AAU66663	Propionibacterium	810	6	1.2	193	22	ABP28957	Protein #1565 enco
738	6	1.2	164	22	AAU66663	S cerevisiae apopt	811	6	1.2	193	22	ABP28957	Human brain expres
739	6	1.2	165	21	AAU66663	Zea mays protein f	812	6	1.2	193	22	AAU54915	Human bone marrow
740	6	1.2	166	22	AAU66663	Novel human enzyme	813	6	1.2	193	22	AAU67296	Human bone marrow

522	1.2	105	22	AAG76799	Human colon cancer	595	6	1.2	122	22	AAU43828	Propionibacterium
523	1.2	105	23	ABP35552	Human ORF4525 prot	596	6	1.2	122	22	ABG02444	Novel human diagno
524	1.2	105	23	ABP03375	Human ORFX protein	597	6	1.2	122	22	ABBI0328	Human cDNA SEQ ID
525	1.2	106	22	AAU64748	Propionibacterium	598	6	1.2	122	22	AAU18491	Human endocrine po
526	1.2	106	22	AAB93551	Human protein sequ	599	6	1.2	122	22	AAW79684	Human protein SEQ
527	1.2	107	10	AAU95449	Sequence encoded b	600	6	1.2	122	22	AAW43570	Human polypeptide
528	1.2	107	22	AAU39627	Propionibacterium	601	6	1.2	122	22	AAB80306	Human prostate can
529	1.2	108	21	AAG39333	Arabidopsis thalia	602	6	1.2	122	22	AAU19671	Human novel extrac
530	1.2	108	22	AAG74393	Human colon cancer	603	6	1.2	122	22	AAU21699	Novel human neopla
531	1.2	109	21	AAG36096	zebra may protein f	604	6	1.2	122	23	ABP47891	Human polypeptide
532	1.2	109	22	AAU50664	Propionibacterium	605	6	1.2	124	21	ABP47891	Arabidopsis thalia
533	1.2	109	22	AAU53521	Propionibacterium	606	6	1.2	124	22	AAU28122	Novel human secret
534	1.2	109	22	ABB27651	Human peptide #302	607	6	1.2	125	17	AAU91230	Rabbit G-protein c
535	1.2	109	22	ABB32821	Human peptide #302	608	6	1.2	125	18	AAW09842	Rabbit G-protein-l
536	1.2	109	22	ABB18303	Protein #302 encod	609	6	1.2	126	16	AAW09842	Human ORF1698 prot
537	1.2	109	22	AAM82096	Human haematologic	610	6	1.2	126	16	AAW09842	African Green Monk
538	1.2	109	22	AAM82096	Human brain expres	611	6	1.2	126	16	AAW09842	Ly-6 terminal CIP
539	1.2	109	22	AAM66007	Human bone marrow	612	6	1.2	126	20	AAW35871	Chlamydia pneumoni
540	1.2	109	22	AAM66007	Human immune/haema	613	6	1.2	126	21	AAW35871	Human secreted pro
541	1.2	109	22	AAU13876	Peptide #310 encod	614	6	1.2	126	21	AAW35871	Arabidopsis thalia
542	1.2	109	22	AAU23852	zebra EST encoded	615	6	1.2	126	21	AAW35871	Arabidopsis thalia
543	1.2	109	22	AAU23852	Peptide #320 encod	616	6	1.2	126	21	AAW35871	Arabidopsis thalia
544	1.2	109	22	AAU01619	Peptide #301 encod	617	6	1.2	126	21	AAW35871	Arabidopsis thalia
545	1.2	109	23	ABG35655	Human peptide enco	618	6	1.2	126	22	ABG35655	Arabidopsis thalia
546	1.2	110	20	AAU43035	Rice serine palmit	619	6	1.2	127	23	ABG35655	Novel human diagno
547	1.2	110	21	AAU43035	Human secreted pro	620	6	1.2	127	23	ABG35655	Novel human diagno
548	1.2	110	22	AAU61823	Propionibacterium	621	6	1.2	128	16	AAW66983	Baboon complement
549	1.2	110	23	ABP04607	Human ORFX protein	622	6	1.2	128	16	AAW66983	Ly-6 terminal CIP
550	1.2	110	23	ABP08577	Human ORFX protein	623	6	1.2	128	21	AAW66983	Human polypeptide
551	1.2	111	18	AAW55458	H. pylori ORF 029p	624	6	1.2	129	22	AAW66983	Arabidopsis thalia
552	1.2	111	20	AAU11884	Human 5' EST seque	625	6	1.2	130	20	AAW66983	Human polypeptide
553	1.2	111	21	AAU52526	Helicobacter pylori	626	6	1.2	130	21	AAW66983	Extended human sec
554	1.2	112	21	AAU52526	Eucalyptus grandis	627	6	1.2	130	21	AAW66983	Arabidopsis thalia
555	1.2	112	21	AAU52526	Arabidopsis thalia	628	6	1.2	130	23	ABP02147	Arabidopsis thalia
556	1.2	112	21	AAU52526	Feline CD40 fragme	629	6	1.2	131	21	AAW66983	Arabidopsis thalia
557	1.2	112	22	AAU60798	Propionibacterium	630	6	1.2	131	22	ABG16171	Human ORFX protein
558	1.2	112	23	ABP42131	Human ovarian anti	631	6	1.2	132	22	AAU63065	Arabidopsis thalia
559	1.2	113	22	ABG16173	Novel human diagno	632	6	1.2	132	22	AAU63065	Propionibacterium
560	1.2	114	21	AAU12767	Arabidopsis thalia	633	6	1.2	132	23	ABP07944	Human novel protei
561	1.2	114	22	ABG3625	Novel human diagno	634	6	1.2	132	23	ABP07944	Human ORFX protein
562	1.2	114	22	ABG3625	Novel human diagno	635	6	1.2	133	22	ABG3625	Human polypeptide
563	1.2	115	21	AAU91642	Human secreted pro	636	6	1.2	133	22	ABG3625	Drosophila melanog
564	1.2	115	21	AAU91642	Human secreted pro	637	6	1.2	133	22	ABG3625	C glutamic prote
565	1.2	115	22	AAU97698	Human secreted pro	638	6	1.2	134	19	AAW62634	Part of a flea ser
566	1.2	115	22	AAU97698	Mouse EGFH2 protei	639	6	1.2	134	21	AAW62634	Human secreted pro
567	1.2	115	23	ABG34892	Neisseria meningit	640	6	1.2	135	21	AAW62634	Arabidopsis thalia
568	1.2	115	23	ABG34892	Human ORF3865 prot	641	6	1.2	135	22	AAW62634	Protein #2968 enco
569	1.2	115	23	ABG34892	Human polypeptide	642	6	1.2	135	22	AAW62634	Peptide #3081 enco
570	1.2	116	22	ABG69805	Mouse pro-NRG-4 am	643	6	1.2	136	21	AAW62634	zebra may protein f
571	1.2	116	22	ABG21774	Drosophila melanog	644	6	1.2	136	22	AAU59501	Propionibacterium
572	1.2	116	22	AAU94582	Novel human diagno	645	6	1.2	136	22	AAU59501	Human polypeptide
573	1.2	116	22	AAU11518	Human protein sequ	646	6	1.2	137	21	AAW44074	Human cancer assoc
574	1.2	116	23	AAU11519	Human fertility-as	647	6	1.2	137	21	AAW44074	Arabidopsis thalia
575	1.2	116	23	AAU11520	Human fertility-as	648	6	1.2	137	21	AAW44074	Arabidopsis thalia
576	1.2	117	21	AAU05056	Human fertility-as	649	6	1.2	138	21	AAW44074	Arabidopsis thalia
577	1.2	117	21	AAU05056	Arabidopsis thalia	650	6	1.2	138	21	AAW44074	Arabidopsis thalia
578	1.2	117	22	AAU70015	Arabidopsis thalia	651	6	1.2	138	21	AAW44074	Anti-human VEGF re
579	1.2	117	22	AAU70015	Drosophila melanog	652	6	1.2	138	22	AAW44074	Human EST encoded
580	1.2	117	22	AAU70015	Propionibacterium	653	6	1.2	138	22	AAW44074	Anti-human Flt-1 m
581	1.2	117	22	AAU70015	Human gene 4 encod	654	6	1.2	140	20	AAW44074	Human normal ovari
582	1.2	117	23	ABG30664	Human gene 13 enco	655	6	1.2	140	21	AAW44074	Human secreted pro
583	1.2	117	23	ABG30664	Human albumin fusi	656	6	1.2	141	21	AAW44074	Arabidopsis thalia
584	1.2	117	23	ABP08729	Human ORFX protein	657	6	1.2	141	22	ABG24105	Arabidopsis thalia
585	1.2	118	21	AAU12766	Arabidopsis thalia	658	6	1.2	142	23	ABP02117	Novel human diagno
586	1.2	118	22	AAU51018	Propionibacterium	659	6	1.2	143	21	AAW44074	Human ORFX protein
587	1.2	118	22	AAU51018	Arabidopsis thalia	660	6	1.2	143	21	AAW44074	Arabidopsis thalia
588	1.2	120	21	ABG42874	Novel human diagno	661	6	1.2	143	22	AAW44074	Novel human diagno
589	1.2	120	21	ABG42874	Arabidopsis thalia	662	6	1.2	144	21	AAW44074	Arabidopsis thalia
590	1.2	120	23	ABP10533	Human DNA polymera	663	6	1.2	145	20	AAW44074	Human pheromone re
591	1.2	121	21	AAU54339	Human ORFX protein	664	6	1.2	145	22	AAU49570	Propionibacterium
592	1.2	121	21	AAU54339	Human pancreatic c	665	6	1.2	145	22	AAU49570	Novel human secret
593	1.2	121	22	AAU54339	Human ORFX ORF2230	666	6	1.2	145	22	AAU49570	Human reproductive
594	1.2	122	21	AAU54339	C glutamic prote	667	6	1.2	146	22	AAU49570	Human breast or ov
	1.2	122	21	AAU54339	Human prostate can		6	1.2	146	22	AAU49570	Drosophila melanog
	1.2	122	21	AAU54339	Arabidopsis thalia		6	1.2	146	22	AAU49570	Drosophila melanog

376	6	1.2	68	21	AAG03055	Human secreted pro	449	6	1.2	88	22	AAU58101	Propionibacterium
377	6	1.2	68	23	ABP07466	Human ORFX protein	450	6	1.2	88	22	AAO13637	Human polypeptide
378	6	1.2	69	21	AAG39334	Arabidopsis thalia	451	6	1.2	88	22	AAW41971	Human polypeptide
379	6	1.2	69	22	AAU52601	Propionibacterium	452	6	1.2	88	23	ABW48668	Listeria monocytog
380	6	1.2	70	21	ABG02382	Novel human diagno	453	6	1.2	89	22	ABW5549	Human albumin fusi
381	6	1.2	71	21	AAG22745	Zea mays protein f	454	6	1.2	89	23	ABG64731	Neisseria mening
382	6	1.2	71	22	AAG33487	Arabidopsis thalia	455	6	1.2	89	23	ABW72918	Drosophila melanog
383	6	1.2	72	21	AAU51740	Propionibacterium	456	6	1.2	90	22	ABW70084	Human colon cancer
384	6	1.2	72	22	AAU52434	Propionibacterium	457	6	1.2	90	22	ABG74248	Drosophila melanog
385	6	1.2	72	22	AAU66096	Peptide #9296 enco	458	6	1.2	91	22	ABW67733	Novel human diagno
386	6	1.2	72	22	ABW41790	Protein #7517 enco	459	6	1.2	91	22	ABG01525	C glutamicum prote
387	6	1.2	72	22	ABW25518	Human brain expres	460	6	1.2	92	21	AAG34719	Arabidopsis thalia
388	6	1.2	72	22	AAW62662	Human bone marrow	461	6	1.2	92	21	AAW77580	Human bone marrow
389	6	1.2	72	22	AAW75480	Peptide #7034 enco	462	6	1.2	92	22	AAW00780	Human 5' EST relat
390	6	1.2	72	22	AAW20600	Peptide #9623 enco	463	6	1.2	93	19	AAW77580	Novel human diagno
391	6	1.2	72	22	AAW35586	Human colon cancer	464	6	1.2	93	21	AAW65015	Novel human diagno
392	6	1.2	72	22	AAW75353	Human peptide enco	465	6	1.2	93	22	ABG10532	Novel human diagno
393	6	1.2	72	23	ABG45041	Propionibacterium	466	6	1.2	93	22	ABG15611	Human polypeptide
394	6	1.2	73	22	AAU62590	Propionibacterium	467	6	1.2	93	23	AAW06744	Human ovarian anti
395	6	1.2	73	22	AAU65472	Propionibacterium	468	6	1.2	93	23	ABW69031	Drosophila melanog
396	6	1.2	73	22	AAW92918	C glutamicum prote	469	6	1.2	94	22	ABW69031	Novel human diagno
397	6	1.2	74	20	AAW25741	Human secreted pro	470	6	1.2	94	22	ABG10742	Zea mays protein f
398	6	1.2	74	23	ABP07579	Human ORFX protein	471	6	1.2	95	21	AAW32798	Arabidopsis thalia
399	6	1.2	75	20	AAW27314	Baboon CD59 protei	472	6	1.2	95	21	AAW32798	Propionibacterium
400	6	1.2	75	22	ABG03850	Novel human diagno	473	6	1.2	95	22	AAU42795	Propionibacterium
401	6	1.2	75	22	ABG10360	Novel human diagno	474	6	1.2	95	22	AAU67212	Novel human diagno
402	6	1.2	75	22	ABG14248	Novel human diagno	475	6	1.2	95	22	ABG09699	Human glutamate re
403	6	1.2	75	22	ABG19650	Novel human diagno	476	6	1.2	95	23	AAW48987	Arabidopsis thalia
404	6	1.2	76	20	AAW01435	Secreted protein e	477	6	1.2	96	21	AAW14994	Human immune/haema
405	6	1.2	76	22	AAW39653	Propionibacterium	478	6	1.2	96	22	AAW84483	Vibrio cholerae ac
406	6	1.2	76	22	AAW90866	Human immune/haema	479	6	1.2	96	23	AAW19525	Listeria monocytog
407	6	1.2	76	23	ABP00922	Human ORFX protein	480	6	1.2	96	23	ABW49014	Propionibacterium
408	6	1.2	77	20	AAW27315	African green monk	481	6	1.2	97	22	AAU53169	Propionibacterium
409	6	1.2	77	21	AAW27169	Zea mays protein f	482	6	1.2	97	22	ABG16475	Novel human diagno
410	6	1.2	77	21	AAW56886	Arabidopsis thalia	483	6	1.2	97	22	ABW10864	Human ovarian and/
411	6	1.2	77	23	ABP39911	Human ORF2884 prot	484	6	1.2	97	22	AAW94672	Human reproductive
412	6	1.2	77	23	ABP10551	Human ORFX protein	485	6	1.2	97	22	AAW94672	Human immune/haema
413	6	1.2	78	22	AAW67847	Propionibacterium	486	6	1.2	97	23	ABW1072	Human ovarian anti
414	6	1.2	79	21	AAW32799	Zea mays protein f	487	6	1.2	97	23	ABW1072	Tick-derived prote
415	6	1.2	79	21	AAW3564	Human colon cancer	488	6	1.2	98	16	AAW69098	Kunitz protease in
416	6	1.2	79	22	AAW59531	Human secreted pro	489	6	1.2	98	16	AAW68039	Human novel secret
417	6	1.2	79	23	ABP01626	Human ORFX protein	490	6	1.2	98	22	AAU16250	Human ORFX protein
418	6	1.2	80	16	AAW74997	E. maxima Em70-1 N	491	6	1.2	98	23	ABP03272	Peptide #2153 enco
419	6	1.2	80	22	AAU39966	Propionibacterium	492	6	1.2	99	22	ABW29502	Human brain expres
420	6	1.2	80	22	AAU40914	Propionibacterium	493	6	1.2	99	22	AAW55472	Human polypeptide
421	6	1.2	80	22	AAU46520	Propionibacterium	494	6	1.2	100	14	AAW44819	Sequence of the ga
422	6	1.2	80	22	AAW07160	Human polypeptide	495	6	1.2	100	21	AAW34718	Arabidopsis thalia
423	6	1.2	81	21	AAW91643	Human secreted pro	496	6	1.2	100	22	AAW44911	Propionibacterium
424	6	1.2	81	22	ABW5769	Drosophila melanog	497	6	1.2	100	22	ABW29057	Novel human diagno
425	6	1.2	81	22	AAU57229	Propionibacterium	498	6	1.2	100	22	ABW34755	Human ORF3728 prot
426	6	1.2	82	20	AAW11880	Human 5' EST secre	499	6	1.2	100	23	ABP00345	Human ORFX protein
427	6	1.2	82	20	AAW13165	Human secreted pro	500	6	1.2	100	23	AAU77466	NAD-dependent 2-hy
428	6	1.2	82	21	AAG00301	Human secreted pro	501	6	1.2	100	23	AAU77466	Arabidopsis thalia
429	6	1.2	82	21	AAW91557	Human secreted pro	502	6	1.2	101	21	AAW14993	Propionibacterium
430	6	1.2	83	21	AAW59180	Arabidopsis thalia	503	6	1.2	101	22	AAU62689	Propionibacterium
431	6	1.2	83	22	AAU63954	Propionibacterium	504	6	1.2	101	22	AAW76383	Human colon cancer
432	6	1.2	83	22	AAU15954	Human novel secret	505	6	1.2	102	20	AAW37894	Amino acid sequenc
433	6	1.2	83	23	ABW97584	Novel human protei	506	6	1.2	102	21	AAW44992	Arabidopsis thalia
434	6	1.2	84	18	AAW55264	H. pylori ORF 06ge	507	6	1.2	102	22	ABW68971	Drosophila melanog
435	6	1.2	84	20	AAW13120	Human secreted pro	508	6	1.2	102	22	AAW07394	Human polypeptide
436	6	1.2	84	21	AAW35192	Zea mays protein f	509	6	1.2	103	22	AAW04892	Human polypeptide
437	6	1.2	85	21	AAW4831	Arabidopsis thalia	510	6	1.2	104	21	AAW12768	Arabidopsis thalia
438	6	1.2	85	22	ABW70952	Drosophila melanog	511	6	1.2	104	21	AAW41177	Zea mays protein f
439	6	1.2	85	22	AAU39202	Propionibacterium	512	6	1.2	104	22	AAW46662	Propionibacterium
440	6	1.2	86	22	AAW83140	Human immune/haema	513	6	1.2	104	22	AAW65657	Human brain expres
441	6	1.2	86	22	AAW75375	Human colon cancer	514	6	1.2	104	22	AAW90223	Human immune/haema
442	6	1.2	87	21	AAW04827	Arabidopsis thalia	515	6	1.2	104	22	AAW38534	Peptide #12571 enc
443	6	1.2	87	21	AAW19718	Arabidopsis thalia	516	6	1.2	104	23	ABW47300	Human peptide enco
444	6	1.2	87	21	AAW56885	Arabidopsis thalia	517	6	1.2	105	21	AAW12806	Arabidopsis thalia
445	6	1.2	87	21	AAW61015	Arabidopsis thalia	518	6	1.2	105	21	AAW16051	Arabidopsis thalia
446	6	1.2	87	23	ABW97911	Human secretory po	519	6	1.2	105	21	AAW17682	Arabidopsis thalia
447	6	1.2	88	21	AAW59792	Arabidopsis thalia	520	6	1.2	105	21	AAW34542	Arabidopsis thalia
448	6	1.2	88	22	AAW56714	Propionibacterium	521	6	1.2	105	22	AAW22401	Human cardiovascul

230	6	1.2	9	17	AAW06996	Synthetic peptide	303	6	1.2	48	21	AAV87940	Murine intracellular
231	6	1.2	9	17	AAW07003	Synthetic peptide	304	6	1.2	48	21	AAV87941	Hamster intracellular
232	6	1.2	9	22	AAU26674	Human Leukocyte An	305	6	1.2	49	20	AAV11838	Human 5' EST secre
233	6	1.2	10	22	AAU27007	Human Leukocyte An	306	6	1.2	50	20	AAU62442	Propionibacterium
234	6	1.2	10	22	AAU26709	Human Leukocyte An	307	6	1.2	51	22	AAU63623	Propionibacterium
235	6	1.2	10	22	AAU26710	Human Leukocyte An	308	6	1.2	51	22	ABU14755	Human nervous syst
236	6	1.2	10	22	AAU27042	Human Leukocyte An	309	6	1.2	52	20	AAV60419	Human normal bladd
237	6	1.2	10	22	AAU27043	Human Leukocyte An	310	6	1.2	52	20	AAU48265	Propionibacterium
238	6	1.2	10	22	AAG95487	Human complementar	311	6	1.2	52	22	AAU53365	Propionibacterium
239	6	1.2	10	22	AAG88080	Saccharomyces cere	312	6	1.2	52	22	AAU59620	Propionibacterium
240	6	1.2	10	22	AAG88081	Saccharomyces cere	313	6	1.2	53	21	AAU40807	Human ORFX ORF571
241	6	1.2	10	22	AAG88082	Saccharomyces cere	314	6	1.2	53	21	AAU41337	Propionibacterium
242	6	1.2	10	22	AAG88083	Saccharomyces cere	315	6	1.2	53	23	ABP31545	Human ORF518 prote
243	6	1.2	10	22	AAG88084	Saccharomyces cere	316	6	1.2	53	23	ABP35065	Human transport pr
244	6	1.2	12	22	AAG88085	Saccharomyces cere	317	6	1.2	54	22	AAU60212	Propionibacterium
245	6	1.2	12	22	AAU47714	Peptide B1.3. Syn	318	6	1.2	54	22	ABU44495	Peptide #12001 enc
246	6	1.2	14	22	AAU97514	Human peptide #789	319	6	1.2	54	22	ABU44495	Protein #9320 enco
247	6	1.2	15	15	AAU47724	HIV epitope #57.	320	6	1.2	54	22	ABU44495	Human musculoskele
248	6	1.2	15	15	AAU44382	Morphinone reducta	321	6	1.2	54	22	ABU44495	Peptide #8526 enco
249	6	1.2	15	15	AAU77467	NAD-dependent 2-hy	322	6	1.2	54	22	ABU44495	Human ORFX protein
250	6	1.2	19	23	AAU10419	PARI pepducin plpa	323	6	1.2	54	22	ABU44495	Propionibacterium
251	6	1.2	21	22	AAU88704	Human interleukin-	324	6	1.2	54	22	ABU44495	Human ORFX protei
252	6	1.2	22	22	AAU74407	H cadherin transme	325	6	1.2	55	22	AAU48999	Staphylococcus aur
253	6	1.2	24	20	AAU13214	Human secreted pro	326	6	1.2	56	22	AAU34269	Human immune/haema
254	6	1.2	27	19	AAU49894	Amino acid sequenc	327	6	1.2	57	23	ABP34138	Human ORF3111 prot
255	6	1.2	27	21	AAU32369	Human ClqRp trypti	328	6	1.2	57	23	AAU58438	Propionibacterium
256	6	1.2	27	22	AAU82194	Human immune/haema	329	6	1.2	59	22	ABU41178	Peptide #8684 enco
257	6	1.2	28	20	AAU88878	Polypeptide fragme	330	6	1.2	59	22	ABU41178	Protein #7203 enco
258	6	1.2	28	22	ABU50944	Human secreted pro	331	6	1.2	59	22	AAU74840	Human bone marrow
259	6	1.2	28	22	AAU72850	Human bone marrow	332	6	1.2	59	22	AAU89001	Human immune/haema
260	6	1.2	28	22	AAU33081	Peptide #7118 enco	333	6	1.2	59	22	AAU34957	Peptide #8994 enco
261	6	1.2	28	23	ABU42680	Human peptide enco	334	6	1.2	59	22	AAU10111	Human ion channel-
262	6	1.2	30	17	AAU98027	Fusogenic peptide	335	6	1.2	59	23	ABU44621	Human peptide enco
263	6	1.2	31	21	AAU51836	Human secreted pro	336	6	1.2	59	23	ABU44621	Human ORFX protein
264	6	1.2	31	21	AAU44702	Human secreted pro	337	6	1.2	60	21	AAU02632	Human secreted pro
265	6	1.2	34	21	AAU32352	Human ClqRp peptid	338	6	1.2	60	22	AAU42670	Propionibacterium
266	6	1.2	34	22	ABU41223	Peptide #8729 enco	339	6	1.2	60	22	ABU16474	Novel human diagno
267	6	1.2	34	22	ABU25229	Protein #7228 enco	340	6	1.2	60	22	ABU28919	Peptide #1570 enco
268	6	1.2	34	22	AAU21168	Human novel foetal	341	6	1.2	60	22	ABU28919	Peptide #1598 enco
269	6	1.2	34	22	AAU62085	Human brain expres	342	6	1.2	60	22	ABU28919	Human nervous syst
270	6	1.2	34	22	AAU74887	Human bone marrow	343	6	1.2	60	22	ABU28919	Human nervous syst
271	6	1.2	34	22	AAU20445	Peptide #6879 enco	344	6	1.2	60	22	ABU28919	Protein #1528 enco
272	6	1.2	34	22	AAU35003	Peptide #9040 enco	345	6	1.2	60	22	AAU94654	Human reproductive
273	6	1.2	34	23	ABU44654	Human peptide enco	346	6	1.2	60	22	AAU54877	Human brain expres
274	6	1.2	38	22	AAU77581	Human colon cancer	347	6	1.2	60	22	AAU67258	Human bone marrow
275	6	1.2	40	22	AAU67460	Peptide derived fr	348	6	1.2	60	22	AAU15102	Peptide #1536 enco
276	6	1.2	41	21	AAU24502	Human secreted pro	349	6	1.2	60	22	AAU27551	Peptide #1588 enco
277	6	1.2	43	23	ABU51038	Human colon specif	350	6	1.2	60	22	AAU02839	Peptide #1521 enco
278	6	1.2	44	20	AAU60437	Human normal bladd	351	6	1.2	60	23	ABU36909	Human peptide enco
279	6	1.2	44	22	AAU36872	Staphylococcus aur	352	6	1.2	60	23	ABU36909	Human ORF58 protei
280	6	1.2	44	22	AAU37426	Human peptide #350	353	6	1.2	61	21	AAU14344	Bovine pancreatic
281	6	1.2	44	22	ABU27699	Human peptide #350	354	6	1.2	61	21	AAU02185	Human secreted pro
282	6	1.2	44	22	ABU32870	Peptide #376 enco	355	6	1.2	61	22	AAU48451	Propionibacterium
283	6	1.2	44	22	ABU34383	Peptide #11359 enc	356	6	1.2	61	22	ABU34904	Human ORF3877 prot
284	6	1.2	44	22	ABU18352	Protein #351 enco	357	6	1.2	62	22	AAU04061	Propionibacterium
285	6	1.2	44	22	ABU26781	Protein #8780 enco	358	6	1.2	62	22	ABU29741	Peptide #2392 enco
286	6	1.2	44	22	AAU53672	Human brain expres	359	6	1.2	62	22	ABU34912	Peptide #2418 enco
287	6	1.2	44	22	AAU64829	Human brain expres	360	6	1.2	62	22	ABU20326	Protein #2325 enco
288	6	1.2	44	22	AAU66056	Human bone marrow	361	6	1.2	62	22	AAU55723	Human brain expres
289	6	1.2	44	22	AAU77579	Human bone marrow	362	6	1.2	62	22	AAU55723	Human bone marrow
290	6	1.2	44	22	AAU13925	Peptide #359 enco	363	6	1.2	62	22	AAU15925	Peptide #2359 enco
291	6	1.2	44	22	AAU21509	Peptide #7943 enco	364	6	1.2	62	22	AAU15925	Peptide #2465 enco
292	6	1.2	44	22	AAU26331	Peptide #368 enco	365	6	1.2	62	22	AAU28428	Peptide #2343 enco
293	6	1.2	44	22	AAU37763	Peptide #11800 enc	366	6	1.2	62	22	ABU37626	Human peptide enco
294	6	1.2	44	22	AAU01668	Peptide #350 enco	367	6	1.2	63	21	AAG36050	Zea mays protein f
295	6	1.2	44	23	ABU35704	Human peptide enco	368	6	1.2	63	22	AAG60726	Human secreted pro
296	6	1.2	44	23	ABU46610	Human peptide enco	369	6	1.2	65	22	AAU56632	Human secreted pro
297	6	1.2	45	9	AAU81952	Probable C-termina	370	6	1.2	65	22	AAU56632	Propionibacterium
298	6	1.2	45	20	AAU45284	Human secreted pro	371	6	1.2	65	22	AAU56632	C glutamicum prote
299	6	1.2	47	21	AAU64794	Human 5' EST relat	372	6	1.2	65	23	ABU05332	Human ORFX protein
300	6	1.2	48	19	AAU21219	Human bcl2 proto-o	373	6	1.2	66	22	ABU35526	Human ORF4499 prot
301	6	1.2	48	21	AAU04829	Arabidopsis thalia	374	6	1.2	67	22	AAU54088	Propionibacterium
302	6	1.2	48	21	AAU87939	Rat intracellular	375	6	1.2	68	20	AAU13085	Human secreted pro

84	7	1.4	282	22	AAU61956	Propionibacterium	157	7	1.4	535	14	AAU42201	Diphtheria toxin (
85	7	1.4	293	22	AAU31016	Novel human secret	158	7	1.4	535	15	AAU44888	Wild-type diphther
86	7	1.4	299	22	AAU87532	Novel central nerv	159	7	1.4	535	16	AAU86825	Diphtheria toxin-
87	7	1.4	299	22	AAU19738	Human novel extrac	160	7	1.4	535	17	AAU86826	Diphtheria toxin (
88	7	1.4	299	23	ABP47958	Human polypeptide	161	7	1.4	535	18	AAU46448	Amino acid sequenc
89	7	1.4	307	20	AAU38843	Neisseria meningit	162	7	1.4	535	18	AAU24876	Diphtheria toxin.
90	7	1.4	313	21	AAU59033	Breast and ovarian	163	7	1.4	535	19	AAU68090	Diphtheria toxin c
91	7	1.4	317	23	ABP91087	Herbicidally activ	164	7	1.4	535	21	AAU97280	Wild type diphther
92	7	1.4	331	20	AAU67889	Human secreted pro	165	7	1.4	535	21	AAU96456	Diphtheria toxin (
93	7	1.4	332	21	AAU60684	Arabidopsis thalia	166	7	1.4	547	21	AAU96854	A. thaliana AS11 m
94	7	1.4	334	21	AAU60683	Arabidopsis thalia	167	7	1.4	560	7	AAU60516	Tox228 diphtheria t
95	7	1.4	336	21	AAU60682	Arabidopsis thalia	168	7	1.4	560	8	AAU70597	Modified diphtheri
96	7	1.4	340	22	ABP70792	Drosophila melanog	169	7	1.4	560	11	AAU06815	Gly(158) Diphtheri
97	7	1.4	341	23	ABP41484	Human ovarian anti	170	7	1.4	567	11	AAU06607	Porcine chondrocyt
98	7	1.4	388	19	AAU98375	H. pylori GHPO 113	171	7	1.4	599	21	AAU49966	Drosophila melanog
99	7	1.4	388	22	AAU35865	Helicobacter pylor	172	7	1.4	614	22	ABP70487	Hybrid protein DAB
100	7	1.4	388	22	AAU36030	Helicobacter pylor	173	7	1.4	619	13	AAU26486	Diphtheria toxin/U
101	7	1.4	401	18	AAU16339	DAB389-SP-Gly fusi	174	7	1.4	637	23	AAU75365	Diphtheria toxin/U
102	7	1.4	401	22	AAU95262	Human protein sequ	175	7	1.4	638	23	AAU75370	Diphtheria toxin/U
103	7	1.4	417	19	AAU54355	47 kD heat shock p	176	7	1.4	641	20	AAU99383	Diphtheria toxin-1
104	7	1.4	417	21	AAU81908	Human Hsp47 protei	177	7	1.4	642	23	AAU75382	Diphtheria toxin/U
105	7	1.4	418	23	AAU75577	Human heat shock p	178	7	1.4	643	23	AAU75390	Diphtheria toxin/U
106	7	1.4	419	21	AAU56928	Human prostate can	179	7	1.4	650	21	AAU31502	Arabidopsis thalia
107	7	1.4	420	22	AAU63605	Propionibacterium	180	7	1.4	652	21	AAU31501	Arabidopsis thalia
108	7	1.4	423	22	AAU689816	C glutamicum prote	181	7	1.4	652	23	AAU75448	Immunotoxin fusion
109	7	1.4	432	21	AAU43633	Amino acid sequenc	182	7	1.4	656	23	AAU75383	Immunotoxin fusion
110	7	1.4	432	21	AAU91341	Group B Streptococ	183	7	1.4	657	23	AAU75389	Diphtheria toxin/U
111	7	1.4	432	22	AAU03611	Group B Streptococ	184	7	1.4	671	19	AAU68500	Hybrid receptor to
112	7	1.4	432	22	AAU03611	Human ovarian anti	185	7	1.4	676	10	AAU93172	Quarter-length hyb
113	7	1.4	432	22	AAU03611	Human ovarian anti	186	7	1.4	676	21	AAU90706	Quarter-length hyb
114	7	1.4	432	19	AAU80217	Streptococcus poly	187	7	1.4	676	22	AAU07526	Diphtheria toxin/B
115	7	1.4	432	21	AAU80217	48 kD modified di	188	7	1.4	693	16	AAU66738	Cytochrome-P450-ox
116	7	1.4	432	21	AAU80217	Arabidopsis thalia	189	7	1.4	724	22	AAU87349	Novel central nerv
117	7	1.4	432	22	AAU80217	Drosophila melanog	190	7	1.4	751	21	AAU31500	Novel central nerv
118	7	1.4	432	22	AAU80217	Modified diphtheri	191	7	1.4	756	22	AAU87329	Arabidopsis thalia
119	7	1.4	432	22	AAU80217	Human protein sequ	192	7	1.4	794	18	AAU25637	Novel central nerv
120	7	1.4	432	22	AAU80217	Human secreted pro	193	7	1.4	794	18	AAU25637	Human cadherin-12
121	7	1.4	432	22	AAU80217	51 kD modified dip	194	7	1.4	805	22	ABP59621	Putative human cad
122	7	1.4	432	22	AAU80217	Modified diphtheri	195	7	1.4	814	22	AAU31501	Drosophila melanog
123	7	1.4	432	22	AAU80217	Human ovarian anti	196	7	1.4	820	22	AAU87115	Human polypeptide
124	7	1.4	432	22	AAU80217	Human STCH chapero	197	7	1.4	820	22	AAU87115	Novel central nerv
125	7	1.4	432	22	AAU80217	Rat STCH chaperone	198	7	1.4	849	22	ABG05943	Novel human diagno
126	7	1.4	432	22	AAU80217	Rat cannabinoide re	199	7	1.4	869	10	AAU93171	Half-length hybrid
127	7	1.4	432	22	AAU80217	Mouse ischaemic co	200	7	1.4	869	21	AAU90705	Half-length hybrid
128	7	1.4	432	22	AAU80217	51 kD modified di	201	7	1.4	869	22	AAU07525	Diphtheria toxin/B
129	7	1.4	432	22	AAU80217	Neisseria meningit	202	7	1.4	885	22	AAU32393	Novel human secret
130	7	1.4	432	22	AAU80217	Neisseria meningit	203	7	1.4	895	23	AAU75368	Diphtheria toxin/U
131	7	1.4	432	22	AAU80217	Neisseria gonorrhoe	204	7	1.4	895	23	AAU75369	Diphtheria toxin/U
132	7	1.4	432	22	AAU80217	Sequence of genet	205	7	1.4	895	23	AAU75374	Diphtheria toxin/U
133	7	1.4	432	22	AAU80217	Arabidopsis acyl C	206	7	1.4	896	23	AAU75366	Diphtheria toxin/U
134	7	1.4	432	22	AAU80217	Arabidopsis diacyl	207	7	1.4	896	23	AAU75367	Diphtheria toxin/U
135	7	1.4	432	22	AAU80217	A. thaliana diacyl	208	7	1.4	899	23	AAU75373	Diphtheria toxin/U
136	7	1.4	432	22	AAU80217	A. thaliana diacyl	209	7	1.4	920	22	ABP65710	Diphtheria toxin/U
137	7	1.4	432	22	AAU80217	Acyl-CoA:cholester	210	7	1.4	1013	22	AAU32392	Drosophila melanog
138	7	1.4	432	22	AAU80217	Arabidopsis thalia	211	7	1.4	1184	20	AAU74445	Novel human secret
139	7	1.4	432	22	AAU80217	Arabidopsis thalia	212	7	1.4	1184	20	AAU74445	Human nucleotide p
140	7	1.4	432	22	AAU80217	Diphtheria toxin (213	7	1.4	1184	22	AAU12377	Membrane-bound pro
141	7	1.4	432	22	AAU80217	Drosophila melanog	214	7	1.4	1184	22	AAU65180	Human PRO1188 poly
142	7	1.4	432	22	AAU80217	Diphtheria toxin d	215	7	1.4	1241	22	AAU25606	Human PRO1188 (UNQ
143	7	1.4	432	22	AAU80217	Diphtheria toxin d	216	7	1.4	1293	22	AAU80214	Human protein sequ
144	7	1.4	432	22	AAU80217	Diphtheria toxin (217	7	1.4	1293	22	AAU80215	Human protein sequ
145	7	1.4	432	22	AAU80217	Diphtheria toxin (218	7	1.4	1323	22	AAU79231	Human protein sequ
146	7	1.4	432	22	AAU80217	Diphtheria toxin (219	7	1.4	1323	23	AAU66142	Human PAS Kinase (
147	7	1.4	432	22	AAU80217	Diphtheria toxin (220	7	1.4	1330	22	AAU79230	Human protein sequ
148	7	1.4	432	22	AAU80217	Diphtheria toxin (221	7	1.4	1330	22	AAU65630	Novel protein kina
149	7	1.4	432	22	AAU80217	Diphtheria toxin (222	7	1.4	1421	21	AAU58573	Sorangium celluloso
150	7	1.4	432	22	AAU80217	Diphtheria toxin (223	7	1.4	1698	22	ABP67538	Drosophila melanog
151	7	1.4	432	22	AAU80217	Diphtheria toxin (224	7	1.4	1828	17	AAU81531	BRCA1 mutant from
152	7	1.4	432	22	AAU80217	Diphtheria toxin (225	7	1.4	2391	15	AAU55694	Carbamoyl-phosphat
153	7	1.4	432	22	AAU80217	Diphtheria toxin (226	7	1.4	2391	15	AAU55694	Bacterial conserve
154	7	1.4	432	22	AAU80217	Native Diphtheria	227	6	1.2	8	22	AAU69062	Human leucocyte an
155	7	1.4	432	22	AAU80217	Cross-reactive mat	228	6	1.2	9	17	AAU49633	Synthetic peptide
156	7	1.4	432	22	AAU80217	Diphtheria toxin f	229	6	1.2	9	17	AAU07037	Synthetic peptide

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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:08:25 ; Search time 40 Seconds
(without alignments)
1665.633 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 500
Sequence: 1 MRGELWLLVLVLRARALS.....YAEVPSGHEKEGFMEEAQC 500

Scoring Table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	500	23	Human Tumour Endot
2	500	100.0	1002	23	Human Tumour Endot
3	371	74.2	400	21	Human ORFX ORF2895
4	271	54.2	431	22	Human endotheial
5	130	26.0	146	23	Human polypeptide
6	108	21.6	205	22	Human immune/haema
7	68	13.6	108	19	Homo sapiens adult
8	68	13.6	108	22	Human CC194.4 prot
9	53	10.6	53	22	Peptide #6597 enco
10	53	10.6	53	22	Human brain expres

11	53	10.6	53	22	AAW72325	Human bone marrow
12	53	10.6	53	22	AAW32584	Peptide #6621 enco
13	53	10.6	53	22	ABG42140	Human peptide enco
14	41	8.2	306	22	ABG09319	Novel human diago
15	35	7.0	500	23	ABG90729	Mouse Tumour Endot
16	35	7.0	500	23	ABG90783	Mouse Tumour Endot
17	13	2.6	1230	22	ABG20074	Novel human diago
18	11	2.2	140	23	ABP05064	Human ORFX protein
19	10	2.0	200	21	AA404099	Human ORFX ORF263
20	10	2.0	392	22	AAW85392	Stem cell growth f
21	10	2.0	392	22	AAW85393	Stem cell growth f
22	10	2.0	425	22	AAW85393	Human polypeptide
23	10	2.0	425	22	AAW85399	Human polypeptide
24	10	2.0	427	22	AAW40853	Human polypeptide
25	10	2.0	427	22	AAW40854	Human polypeptide
26	10	2.0	449	22	AAW85398	Stem cell growth f
27	10	2.0	486	22	AAW39067	Human polypeptide
28	10	2.0	499	22	AAW85396	Human polypeptide
29	10	2.0	529	22	AAU29259	Human PRO polypept
30	10	2.0	529	22	AAW39068	Human polypeptide
31	10	2.0	529	22	AAW85394	Stem cell growth f
32	10	2.0	529	22	AAW85394	Stem cell growth f
33	10	2.0	529	22	ABG31211	Amino acid sequenc
34	10	2.0	529	23	ABG90726	Human Tumour Endot
35	10	2.0	530	23	ABG90734	Human Tumour Endot
36	10	2.0	530	23	ABG90784	Mouse Tumour Endot
37	8	1.6	68	23	ABP02478	Human ORFX protein
38	8	1.6	107	23	ABP02121	Human ORFX protein
39	8	1.6	169	22	ABW52628	Escherichia coli p
40	8	1.6	460	23	ABP25434	Streptococcus poly
41	8	1.6	625	22	ABW58966	Drosophila melanog
42	8	1.6	924	22	ABG17498	Novel human diago
43	7	1.4	11	20	AAW97291	Cyclosporin A muta
44	7	1.4	68	22	AAW45082	Propionibacterium
45	7	1.4	73	21	AAW35583	Arabidopsis thalia
46	7	1.4	74	19	AAW75218	Human secreted pro
47	7	1.4	75	22	AAW98446	Human papillomavir
48	7	1.4	77	22	ABW43890	Peptide #11396 enc
49	7	1.4	77	22	AAW64880	Human brain expres
50	7	1.4	80	23	ABP01768	Human ORFX protein
51	7	1.4	89	23	ABP07835	Human ORFX protein
52	7	1.4	96	20	AAW45144	pGR2P13 protein se
53	7	1.4	99	22	ABW5527	Human secreted pro
54	7	1.4	99	23	ABG64709	Human albumin fusi
55	7	1.4	110	21	AAW14306	Human secreted pro
56	7	1.4	110	21	AAW14306	Human secreted pro
57	7	1.4	110	22	AAW85543	Human secreted pro
58	7	1.4	110	22	AAW85528	Human secreted pro
59	7	1.4	110	23	ABG64708	Human albumin fusi
60	7	1.4	112	22	AAW24374	Human EST encoded
61	7	1.4	114	22	AAW03642	Propionibacterium
62	7	1.4	116	17	AAW03642	Human cannabinoid
63	7	1.4	119	21	AAW20095	protein encoded by
64	7	1.4	120	20	AAW45143	pGR2P16 protein se
65	7	1.4	129	22	AAW46336	Propionibacterium
66	7	1.4	131	22	ABG10014	Novel human diago
67	7	1.4	136	22	AAU32938	Novel human secret
68	7	1.4	151	22	AAW92871	Human protein sequ
69	7	1.4	157	22	AAW01044	Human polypeptide
70	7	1.4	157	22	AAW01465	Human polypeptide
71	7	1.4	178	22	AAU19300	Human G protein-co
72	7	1.4	193	18	AAW24877	Diphtheria toxin f
73	7	1.4	213	21	AAW43148	Human ORFX ORF2912
74	7	1.4	213	22	AAW93671	Human protein sequ
75	7	1.4	217	22	AAW93684	Human protein sequ
76	7	1.4	225	19	AAW44944	Drosophila melanog
77	7	1.4	225	19	AAW44944	Avian infectious b
78	7	1.4	225	22	AAW62815	E. canis protein a
79	7	1.4	229	22	AAU56832	Propionibacterium
80	7	1.4	260	22	ABW63338	Drosophila melanog
81	7	1.4	267	22	ABG03238	Novel human diago
82	7	1.4	270	22	AAW92214	C glutamic prote
83	7	1.4	274	22	AAW25617	Human protein sequ
84	7	1.4	274	22	AAW74275	Human colon cancer

FT Peptide 1...100
 FT /note= "predicted signal/leader peptide"
 XX WO9814576-A2.
 PN 09-APR-1998.
 XX 03-OCT-1997; 97WO-US18007.
 PD 04-OCT-1996; 96US-0726237.
 XX (GEMY) GENETICS INST INC.
 XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX WPI; 1998-240082/21.
 DR N-PSDB; AAV11619.
 XX Nucleic acids encoding novel secreted proteins - useful as, e.g.
 XX anti-inflammatory, immuno-stimulatory or suppressing agents
 XX Disclosure; Page 79; 110pp; English.
 XX The sequence is that of a secreted protein encoded by
 CC an isolated polynucleotide which may be of use in the
 CC production of therapeutic compositions for treating or
 CC ameliorating a medical condition in a mammal. Such compositions
 CC may be used for, e.g. research purposes as markers for
 CC tissues, molecular weight markers for gels, primers or probes, for
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be
 CC used as a cytokine for cell proliferation and differentiation activity,
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal
 CC infections, for autoimmune diseases such as multiple sclerosis or
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue
 CC growth, as an activator or inhibitor, or as a chemotactic or
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,
 CC anti-inflammatory or tumour inhibitor agents.
 XX Sequence 108 AA;
 SQ
 Query Match 13.6%; Score 68; DB 19; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.3e-60;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 383 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVIGIVLAVLLVAAIL 442
 DB 41 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVIGIVLAVLLVAAIL 100
 QY 443 AGIYINGH 450
 DB 101 AGIYINGH 108
 RESULT 8
 AAB90677
 ID AAB90677 standard; Protein; 108 AA.
 XX AAB90677;
 AC
 XX 07-JUN-2001 (first entry)
 DT
 XX Human CC194_4 protein sequence SEQ ID 30.
 DE
 XX Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW haematopoiesis.
 XX
 OS Homo sapiens.
 XX
 XX WO200119988-A1.
 PN
 XX

PD 22-MAR-2001.
 XX
 PF 14-SEP-2000; 2000WO-US25135.
 XX
 PR 17-SEP-1999; 99US-0398829.
 XX
 XX (GEMY) GENETICS INST INC.
 XX
 XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MK, Spaulding V, Agostino MJ;
 XX WPI; 2001-244801/25.
 DR N-PSDB; AAF98392.
 XX Isolated nucleic acids encoding polypeptides, useful for modulating
 XX e.g. cytokine and cell proliferation/differentiation activity, the
 XX immune system and hematopoiesis regulating activity -
 XX Disclosure; Page 399; 557pp; English.
 XX Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; receptor/ligand activity; anti-inflammatory activity; and/or
 CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
 CC tumour inhibition activity. Included in the invention are probes
 CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
 CC encoding the secreted proteins.
 XX Sequence 108 AA;
 SQ
 Query Match 13.6%; Score 68; DB 22; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.3e-60;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 383 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVIGIVLAVLLVAAIL 442
 DB 41 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVIGIVLAVLLVAAIL 100
 QY 443 AGIYINGH 450
 DB 101 AGIYINGH 108
 RESULT 9
 ABB39091
 ID ABB39091 standard; Peptide; 53 AA.
 XX
 AC ABB39091;
 XX
 XX 04-FEB-2002 (first entry)
 DT
 XX Peptide #6597 encoded by human foetal liver single exon probe.
 DE
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW
 XX Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00669.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 PR

PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 PT
 XX Claim 27; SEQ ID NO 31726; 639pp + sequence listing; English.
 PS
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 53 AA;
 Query Match 10.6%; Score 53; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 HDEGPGSGWAAKGTGVRGWNRRRARESPGHVSEPDRTQLSQDLGGGTAMDITLPD 79
 DB 1 HDEGPGSGWAAKGTGVRGWNRRRARESPGHVSEPDRTQLSQDLGGGTAMDITLPD 53
 RESULT 10
 AAM59743
 ID AAM59743 standard; Protein; 53 AA.
 AC AAM59743;
 XX
 XX 05-NOV-2001 (first entry)
 DT Human brain expressed single exon probe encoded protein SEQ ID NO: 31848.
 DE Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer.
 XX Homo sapiens.
 OS
 XX WO200157275-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00667.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483446/52.
 DR

XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 PT
 XX Example 4; SEQ ID NO: 31848; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX
 SQ Sequence 53 AA;
 Query Match 10.6%; Score 53; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 HDEGPGSGWAAKGTGVRGWNRRRARESPGHVSEPDRTQLSQDLGGGTAMDITLPD 79
 DB 1 HDEGPGSGWAAKGTGVRGWNRRRARESPGHVSEPDRTQLSQDLGGGTAMDITLPD 53
 RESULT 11
 AAM72325
 ID AAM72325 standard; Protein; 53 AA.
 AC AAM72325;
 XX
 XX 06-NOV-2001 (first entry)
 DT Human bone marrow expressed probe encoded protein SEQ ID NO: 32631.
 DE Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.
 OS
 XX WO200157276-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00668.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 PT
 XX Example 4; SEQ ID NO: 32631; 658pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 SQ Sequence 53 AA;

Query Match
Best Local Similarity 10.6%; Score 53; DB 22; Length 53;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 HDEGPGGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 79
DB 1 HDEGPGGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 53

RESULT 12
AA332584
ID AAM32584 standard; Protein; 53 AA.
AC AAM32584;
XX
XX
XX 17-OCT-2001 (first entry)
XX
XX Peptide #6621 encoded by probe for measuring placental gene expression.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200157272-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00663.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
XX Claim 27; SEQ ID No 32853; 654pp; English.
PS
XX
XX The present invention relates to single exon nucleic acid probes (SENPs;
CC see AA13315-AA157346). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
XX Sequence 53 AA;
SQ

Query Match
Best Local Similarity 10.6%; Score 53; DB 22; Length 53;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 HDEGPGGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 79
DB 1 HDEGPGGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 53

RESULT 13
ABG42140
ID ABG42140 standard; Peptide; 53 AA.
XX
XX
AC ABG42140;

XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31805.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX
XX WO200186003-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00665.
PF
XX
XX 04-FEB-2000; 2000US-180312P.
PR
XX 26-MAY-2000; 2000US-207456P.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-234687P.
PR
XX 27-SEP-2000; 2000US-236359P.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 27; SEQ ID No 31805; 634pp; English.
PS
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridize at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridization of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary

CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 53 AA;

Query Match 10.6%; Score 53; DB 23; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 HDEGPGSGAAKGTVRGNNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTLPD 79
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 HDEGPGSGAAKGTVRGNNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTLPD 53

RESULT 14
 ABG09319
 ID ABG09319 standard; Protein; 306 AA.

XX AC ABG09319;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #9310.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB; AAS73506.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 20; SEQ ID No 39678; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 306 AA;

Query Match 8.2%; Score 41; DB 22; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.8e-32;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 FIFMGDVIIRMLTATQYVAPLMAENPGYSDNSTVVYFDNG 198
 ||||||||||||||||||||||||||||||||||||||||||||||||
 DB 47 FIFMGDVIIRMLTATQYVAPLMAENPGYSDNSTVVYFDNG 87

RESULT 15

ABB90729
 ID ABB90729 standard; Protein; 500 AA.

XX AC ABB90729;

XX DT 30-MAY-2002 (first entry)

XX DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.

XX OS Mus musculus.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US24031.

XX PR 02-AUG-2000; 2000US-222599P.

XX PR 11-AUG-2000; 2000US-224360P.

XX PR 11-APR-2001; 2001US-282850P.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2002-291856/33.

XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth

XX Disclosure; Page 146-147; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.

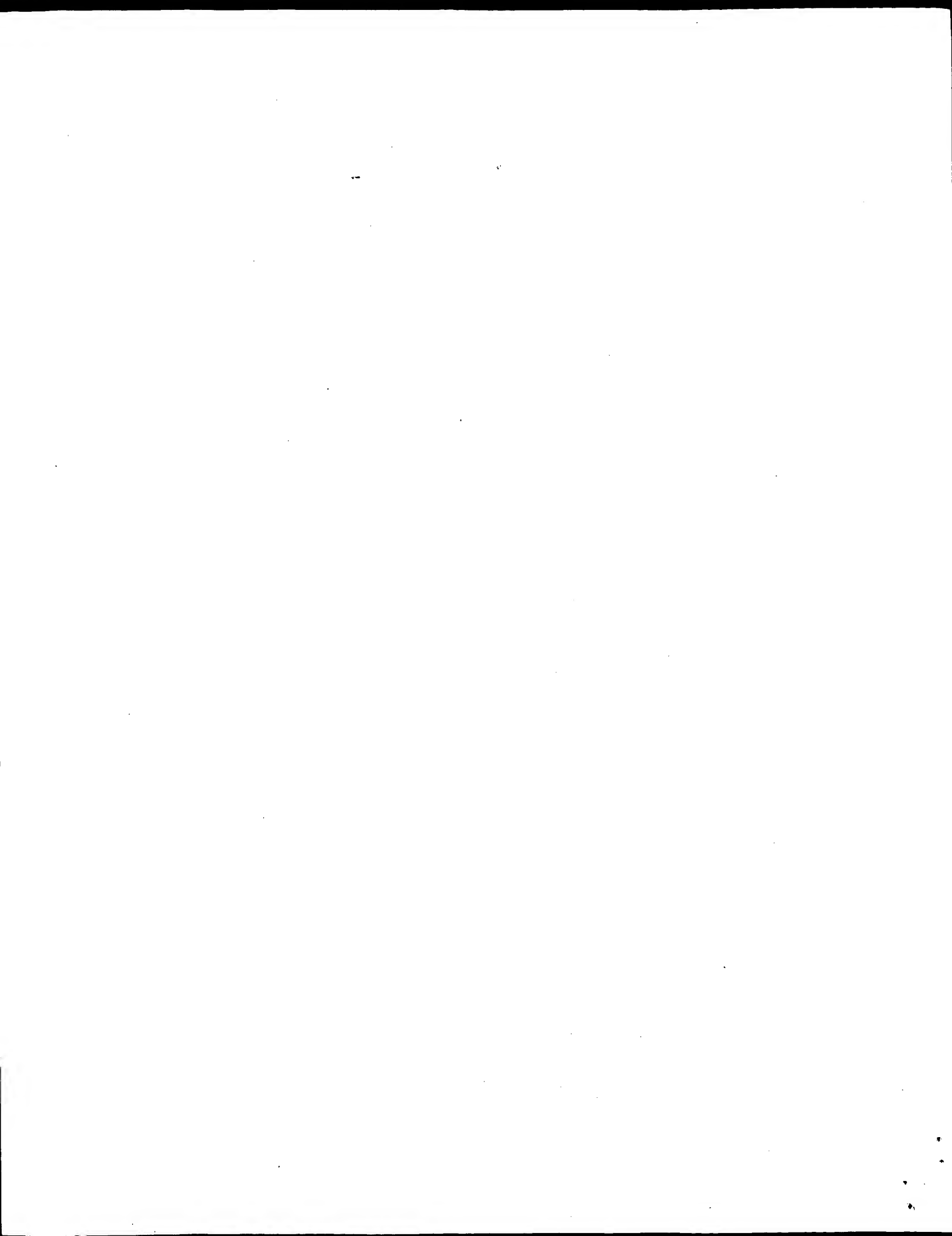
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SQ Sequence 500 AA;

Query Match 7.0%; Score 35; DB 23; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HRQASRVVLSFDPFYGHPLRQITITATGGFIFMGD 163
 ||||||||||||||||||||||||||||||||||||
 Db 130 HRQASRVVLSFDPFYGHPLRQITITATGGFIFMGD 164

Search completed: April 22, 2003, 16:16:53
 Job time : 67 secs



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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:05:15 ; Search time 16 seconds
(without alignments)
919.466 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115.5	4.3	1568	US-09-181-706-2	Sequence 2, Appl
2	115.5	4.3	1568	US-09-458-791-2	Sequence 2, Appl
3	115.5	4.3	1568	US-09-459-066-2	Sequence 2, Appl
4	95.5	3.5	3052	US-08-557-122A-26	Sequence 26, Appl
5	95.5	3.5	3052	US-09-262-666-26	Sequence 26, Appl
6	93	3.5	1085	US-08-431-080-28	Sequence 28, Appl
7	93	3.5	1085	US-08-938-534-28	Sequence 28, Appl
8	93	3.5	1085	US-09-345-294-28	Sequence 28, Appl
9	92.5	3.4	1220	US-08-158-232-43	Sequence 43, Appl
10	92.5	3.4	1220	US-08-611-928-43	Sequence 43, Appl
11	92.5	3.4	1220	US-09-173-891-43	Sequence 43, Appl
12	90.5	3.4	424	US-08-484-993B-18	Sequence 18, Appl
13	90.5	3.4	424	US-08-484-158B-18	Sequence 18, Appl
14	90.5	3.4	424	US-08-484-596A-18	Sequence 18, Appl
15	90.5	3.4	424	US-08-480-150A-18	Sequence 18, Appl
16	90.5	3.4	424	US-08-458-731-18	Sequence 18, Appl
17	90.5	3.4	424	US-08-149-223A-18	Sequence 18, Appl
18	89.5	3.3	424	5169835-6	Patent No. 5169835
19	89	3.3	595	US-08-232-087A-2	Sequence 2, Appl
20	89	3.3	595	US-09-006-353A-9	Sequence 9, Appl
21	89	3.3	595	US-08-573-986-9	Sequence 9, Appl
22	88.5	3.3	15281	US-08-471-119A-2	Sequence 2, Appl
23	88	3.3	595	US-08-225-989-2	Sequence 2, Appl
24	88	3.3	595	US-08-570-923-2	Sequence 2, Appl
25	88	3.3	595	US-08-580-014-2	Sequence 2, Appl
26	88	3.3	595	US-08-079-785-2	Sequence 2, Appl
27	88	3.3	606	US-09-041-236-4	Sequence 4, Appl

28 87.5 3.3 659 4 US-09-562-737-13 Sequence 13, Appl
29 87.5 3.3 1969 3 US-08-836-325-16 Sequence 16, Appl
30 87.5 3.3 2133 4 US-09-523-656-30 Sequence 30, Appl
31 86.5 3.2 739 1 US-07-618-946B-22 Sequence 22, Appl
32 86.5 3.2 814 1 US-07-618-946B-23 Sequence 23, Appl
33 86 3.2 398 1 US-08-091-519-2 Sequence 2, Appl
34 86 3.2 398 1 US-08-442-043A-2 Sequence 2, Appl
35 86 3.2 398 4 US-09-173-151A-26 Sequence 26, Appl
36 86 3.2 398 5 PCT-US91-03478-2 Sequence 2, Appl
37 85.5 3.2 284 2 US-08-424-641B-2 Sequence 2, Appl
38 85.5 3.2 284 2 US-08-820-980-2 Sequence 2, Appl
39 85.5 3.2 284 2 US-08-826-439-2 Sequence 2, Appl
40 85.5 3.2 349 4 US-09-161-241-8 Sequence 8, Appl
41 85.5 3.2 834 3 US-08-539-205A-6 Sequence 6, Appl
42 84.5 3.1 1984 3 US-08-836-325-10 Sequence 10, Appl
43 84.5 3.1 1989 3 US-08-836-325-12 Sequence 12, Appl
44 84 3.1 572 6 5256770-7 Patent No. 5256770
45 84 3.1 575 1 US-08-312-870-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-181-706-2

; Sequence 2, Application US/09181706

; Patent No. 6130068

; GENERAL INFORMATION:

; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,

; APPLICANT: Robert F. DuBoise, Richard S. Johnson

; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN

; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janis C. Henry

; STREET: 51 University St.

; CITY: Seattle

; STATE: WA

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/181,706

; FILING DATE: October 28, 1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/958,598 (converted to a

; APPLICATION NUMBER: Provisional, see below)

; FILING DATE: October 28, 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598

; APPLICATION NUMBER: conversion to Provisional application)

; FILING DATE: October 26, 1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Henry, Janis C

; REGISTRATION NUMBER: 34,347

; REFERENCE/DOCKET NUMBER: 2631-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)470-4189

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1568 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-181-706-2

Query Match
Best Local Similarity 4.3%; Score 115.5; DB 4; Length 1568;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

US-09-458-791-2

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match
Best Local Similarity 4.3%; Score 115.5; DB 4; Length 1568;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

US-09-458-791-2

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-459-066-2

Query Match 4.3%; Score 115.5; DB 4; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.047;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

QY 39 CTVGRNRRARESPGHVSEPDRT-----QLSDLGGLTAMDLTLPDNRTRVVEDNHSYVVS 94
Db 256 GAATGWPSMAR-----IAQSEVLFGQASLDCGHG-----PDGR-----R 292
QY 95 RLYGSEPHSRELWVAV--AFANRSQVKIHTI-----LSNTHRAQSRVLSF----- 139
Db 293 LLLSSSLVEALDVWAGVFAAGEGQERRSPTTALCLFRMSEIQARAKRVSWDFKTAES 352
QY 140 -----DEFEYGHPLRLQITATGGFTFMGSDVTHRLMTATQYVAPLMAFNPGYSDNSTVYV 194
Db 353 HCKEQDQERVPQIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391
QY 195 FDNQTFVYVQWHDVYVLOGWEDKGSFTFOAALHHDGRI--VPAYKEIPMSVPEI---SSSQ 249
Db 392 LGTG-----DQQLKVLILGENILTSNCPVEIYEKEE 422
QY 250 HPVKTGLSDAPMLNPSDPVPSRRRSIFEVHRIELDPKVTMSAVEFTPLPTCLOHRS 309
Db 423 TPV-----FYKLVPDP-----VKNIIY-----LTAGKEVRRIRVANCNKHS. 460
QY 310 CDACMSSDLTFCNSCHVLCORCSSGFORYOE-----NWDYCAQAEACRCWCEDFQ-----D 361
Db 461 CSECLTA-TDPCGGMQLQKCTFGQDCVHSENLENMLDI-----SSGAKKCPKIQTIRSS 515
QY 362 EDHDSASPTSFSP 375
Db 516 KEKTTVTWVGSFSP 529

RESULT 4
US-08-557-122A-26
Sequence 26, Application US/08557122A
Patent No. 5879664
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Molland
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5879664o No. 5879664disk of No. 5879664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 3052 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-557-122A-26

Query Match 3.5%; Score 95.5; DB 2; Length 3052;
Best Local Similarity 18.5%; Pred. No. 13;
Matches 88; Conservative 52; Mismatches 190; Indels 145; Gaps 17;

QY 80 NRTVRVEDNHSYVRYLGPSEPHSREL---WVDVAEANRSPQVKIHTILSNTHRAQ---- 132
Db 2396 NFEVAFDEKKNVFEFYAPWCCHCKOLAPWDKLGKETKHEODI-VIAKNFEVAFDEN 2454
QY 133 SRVLSFDEFPYGHPLRLQITATGGFTFMGSDVTHRLMTATQYVAPLMAFNPGYSDNSTV 192
Db 2455 KNVFEFYAPWCCH-----CKQLAPAWDKLGPYRDHENI 2489
QY 193 VYFNGTGVVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEI-----PMSVP 243
Db 2490 VIAKN-----HDEIVNDPKDVLVLYAPWCCHCKRLAPTYQELADTYANATSDVLA 2542
QY 244 EISSQHPVKTGLSDAPMLNPSDPVPSRRRSIFEYH-----RI 283
Db 2543 KMDSTANEVAVKVSFPTLK---FFPASADRTVIDYNGERTLDGPKFLESGGMDSTAN 2599
QY 284 ELDPKSVTMSAVEFTPLPTCLOHRSQDCAQMSDLT---FNCWCHVLCORCSSGFORYO 340
Db 2600 EVEAVKHVSFPTLKFP-----ASADRTVIDYNG-----BRTLDGFKKFL 2640
QY 341 EMWDYCAQAEACRCWCEDFQDEHDSASPTSFSPYDGLTTTSSSLFIDSUTTEDDTKL 400
Db 2641 SGGMDSTANEVAVKVSFPTLKFPASADRTVIDYNGERTLDGFKKFL 2691
QY 401 NPYAGGDLGNLNS-----PKTKGTPVHILGTIVGIVLAVLLVLAIIAGIYINGHPTS 453
Db 2692 ---GGMDSTANEVAVKVSFPTLKFPAGPGRTV-----IDYNGERTL 2732
QY 454 NAALFFIER-----RPHHWPAKFRSHPDHSTYAEVPSGHEK-EGF 494
Db 2733 DGFKFLKESGGMDSTANEVAVKVSFPTLKFPAGPGRTV-----IDYNGERTL 2785

RESULT 5
US-09-262-666-26
Sequence 26, Application US/09262666
Patent No. 6346244
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Molland
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6346244o No. 6346244disk of No. 6346244th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,666
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,122
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:

```

; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3980.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3052 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-262-666-26

Query Match 3.5%; Score 95.5; DB 4; Length 3052;
Best Local Similarity 18.5%; Pred. No. 13; Mismatches 190; Indels 145; Gaps 17;
Matches 88; Conservative 52;

QY 80 NRTVRVEDNHSYVSRLYGFPSEPHSREL---WVDVAENRQVKIHTILSNTHRQA--- 132
DB 2396 NFEVAFDEKKNVEFYAPWCGHCKGLAPWDKLGTYKEHQDI-VIAKNFEVAFDEN 2454
QY 133 SRVLSDFDFPYGHPRLQIITAGGFTFMGDVHRMLTATQYVAPLMANFPGYSNSTV 192
DB 2455 KNVFEFYAPWCGH---CKQLAPAWDKLPGTYRDHENI 2489
QY 193 VYFONGTVFVVOVDHVVYLOGWEDKGSFTFOALHHDGRIVFAFKEI-----PMSVP 243
DB 2490 VIAKN-----HDEIVNDPKDVLVLYYAPWCGHCKRLAPYQELADYANTSDVLIA 2542
QY 244 EISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEVH-----RI 283
DB 2543 KMDSTANEVAVKHSEFTLTK---FFPASADRTVIDYNGERTLDGFKFLESGGMDSTAN 2599
QY 284 ELDSKVTSMASAVEFTPLTCLQHRSCDACMSSDLT---FNCWCHVLCRCSSGFDYRQ 340
DB 2600 EVEAVKHSEFTLTKFPF-----ASADRTVIDYNG-----ERTLDGFKFLE 2640
QY 341 EMDYGCQAQAEGRMCDFQDEHDSDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKL 400
DB 2641 SGGMDSTANEVAVKHSEFTLTKFPASADRTVIDYNGERTLDGFKFLES-----2691
QY 401 NPYAGGDLQNNLS-----PKTKGTFVHLGTIVGLVAVLLAAILAGIYINGHPTS 453
DB 2692 ---GGMDSTANEVAVKHSEFTLTKFPAGPGRTV-----IDYNGERTL 2732
QY 454 NAALFFIER-----RPHHPAMKFRSHPDHSTYAEVPSGHEK-EGF 494
DB 2733 DGFKKFLESGGMDSTANEVAVKHSEFTLTKF---FPAGSRNVIDYNGERTLEGF 2785

RESULT 6
US-08-431-080-28
; Sequence 28, Application US/08431080
; Patent No. 5698686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,080
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SN 08/326,781
; FILING DATE: October 20, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1085 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-431-080-28

Query Match 3.5%; Score 93; DB 1; Length 1085;
Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY 56 SPDRTOISQDLGGGTFLAMDTPDNRTVRVEDNHSYVSRLYGFPSEPHSRELWVD--VAE 113
DB 333 NEDSGEIGTDLETGE---DDLPL-----ILLEEQNIIVSEL-----QNDELSPDGSIH 379
QY 114 ANRSQVK---IHTILSNTHRQAS-----RVVLSDFDFPYGHPRLQIITAGGFTFM 161
DB 380 EGSDPVEDAENKFLQNEYNQENGYDEDEDEIMSDFMPEYEDP-----KFNALYY 433
QY 162 GDVHRMLTATQYVAPLMAN-----FNPQYSDNST 191
DB 434 GDSGEPKLSLSL-PLMLNDEKLSKLKKEAKREQERKQRLKLYKKTKPSTRITSN 492
QY 192 VYFONGTVFVVOVDHVVYLOGWEDKGSFTFOALHHDGRIVFAFKEI-----EIPMSVPEISS 247
DB 493 V---DNDEYIF---NVFQSDDENSGHKKGRKSHIEHKNGSNLKSNDLLEP 545
QY 248 SQHP--VKTGLSDAFMILNPSDPVPSRRRSIFEVHRIELDPKSVTSMASAVEFTPLTCL 305
DB 546 STHSTVLNSGKYDS---SDD-----EYDNLDD-----VAHMP-----575
QY 306 QHRSCDACMSSDLTFCNSWCHVLCRCSSGFDYRQEWMDYGCQAQAEGRMCDFQDEHD 365
DB 576 ---SDDECESETSHTADTDELRALDS-----DSLDTG-----ELDDYEDDDDD 619
QY 366 SA-----SPTSFSFYDGO---LTTTSSS-----LFDLSL 392
DB 620 SSVTVNVIDDLDLDFDSFYHYDSDGSSSLSSNSDKNSDKCKKHDLLETVYVVDDE 679
QY 393 TTEDDTKLPYAGGDLQNNLSPKTKG-----TPVHLGT 426
DB 680 STDEDDNLPP---PSRSKNIGSKAKEIVSSNVVGLRPPKLG 719

RESULT 7
US-08-938-534-28
; Sequence 28, Application US/08938534
; Patent No. 5916752
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

```

```

: CITY: Houston
: STATE: TEXAS
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/938,534
: FILING DATE: 26-SEP-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,080
: FILING DATE:
: APPLICATION NUMBER: SN 08/326,781
: FILING DATE: October 20, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Parker, David L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: ARCD:155/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: LENGTH: 1085 amino acids
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-938-534-28

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Query Match 3.5%; Score 93; DB 2; Length 1085;

Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

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QY 56 SEPDRTQLSODLGGGTAMDTLPDNKTRVVDNHSYVSRLYGPPSEPHSRELWVD--VAE 113
Db 333 NEDSHGEIGTDLETGE---DDLPL-----ILEEEQNIVSEL-----QNDDELSDGSIHE 379
QY 114 ANRSQVK--IHTILSNTHRQAS-----RVVLSDFPFYGHPLRQITATGGGIFM 161
Db 380 EGSDPVEDAEKNFLQNEYNQENGDEDEDEIMSDFMPEYEDP-----KFNALYY 433
QY 162 GDVHRMLTATQYVAPLMA-----FNPGYSDNST 191
Db 434 GDGSEPKLSLSTSL-PLMLNDEKLSKLKKEAKKREQERKORRKLKTKQKSTRRTSN 492
QY 192 VVVFONGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYK---EIPMSVPEISS 247
Db 493 V---DNDEYIF---NVFFQSDDENSGHKKGRHKSKEHIEHNKNSLNKSNDDLEP 545
QY 248 SQHP--VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVKTSMSAVEFTPLPTCL 305
Db 546 STHSTVLNSGKYDS-----SDD-----EYDNILLD-----VAHMP----- 575
QY 306 QHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQREWMDYCAQAEGRMCEDFODEDHD 365
Db 576 ---SDDECESESHDADTDEELRALDS-----DSLIDGT-----ELDDYEDDDDD 619
QY 366 SA-----SPDTSFSPYDGD---LTTSSS-----LFIDSL 392
Db 620 SSVTVNFDIDDLDPDSFYHVDSDGSSLSLSSNDSKNSGSKCKKHDLLETVVVYVDE 679
QY 393 TTEDDTKLNPYAGGGLQNNLSPKTKG-----TPVHLGT 426
Db 680 STDEDDNLPP---PSSRSKNIGSKAKIEIVSSNVVGLRPPKLT 719

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RESULT 8

US-09-345-294-28

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: Sequence 28, Application US/09345294
: Patent No. 6387619
: GENERAL INFORMATION:
: APPLICANT: Gottschling, Daniel E.
: SINGER, Miriam S.
: TITLE OF INVENTION: Telomerase Compositions and Methods
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TEXAS
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/345,294
: FILING DATE: 30-Jun-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,080
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Parker, David L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: ARCD:155/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1085 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 28:
: US-09-345-294-28

```

Query Match 3.5%; Score 93; DB 4; Length 1085;
Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

```

QY 56 SEPDRTQLSODLGGGTAMDTLPDNKTRVVDNHSYVSRLYGPPSEPHSRELWVD--VAE 113
Db 333 NEDSHGEIGTDLETGE---DDLPL-----ILEEEQNIVSEL-----QNDDELSDGSIHE 379
QY 114 ANRSQVK--IHTILSNTHRQAS-----RVVLSDFPFYGHPLRQITATGGGIFM 161
Db 380 EGSDPVEDAEKNFLQNEYNQENGDEDEDEIMSDFMPEYEDP-----KFNALYY 433
QY 162 GDVHRMLTATQYVAPLMA-----FNPGYSDNST 191
Db 434 GDGSEPKLSLSTSL-PLMLNDEKLSKLKKEAKKREQERKORRKLKTKQKSTRRTSN 492
QY 192 VVVFONGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYK---EIPMSVPEISS 247
Db 493 V---DNDEYIF---NVFFQSDDENSGHKKGRHKSKEHIEHNKNSLNKSNDDLEP 545
QY 248 SQHP--VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVKTSMSAVEFTPLPTCL 305
Db 546 STHSTVLNSGKYDS-----SDD-----EYDNILLD-----VAHMP----- 575
QY 306 QHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYQREWMDYCAQAEGRMCEDFODEDHD 365
Db 576 ---SDDECESESHDADTDEELRALDS-----DSLIDGT-----ELDDYEDDDDD 619
QY 366 SA-----SPDTSFSPYDGD---LTTSSS-----LFIDSL 392

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: 86Q3
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 86Q3C
US-08-611-928-43

Query Match 3.4%; Score 92.5; DB 2; Length 1220;
Best Local Similarity 20.7%; Pred. No. 6.1;
Matches 74; Conservative 37; Mismatches 108; Indels 139; Gaps 18;

QY 20 SPQAGHDEGPGSGW---AAKGTGVRGNRRARESPGHVSEPDRTQISDGLGGTL-AMD 75
DB 442 TPQGA-----SGWNTNLMRGVSGLSFLQR-----DGTSLSAGMGGGFADTIY 485

QY 76 TLPDNRTRVVDNHSYVSRLYG---PSEPHSRELWVDVAEANKRSQVKIHTLSNTHRQ 131
DB 486 SLP-----ATHYLSYLYGTPYQTSNYSYGHVGVSTPQEAATLPNII-----529

QY 132 ASRVVLSFDFPYGHPLRQITATGGIFM-----GDVIHRLMTATQYVAPLMANFNG- 185
DB 530 -----GQDEQGNVSTMGFFPEKASYGTVVKEWLNANAM-----KLSPGQ 571

QY 186 -----YSDNSTVYVFDNGTVFVQWDHVLQGWEDKG-----SF 219
DB 572 SIGIPITNVTKHNYQVRCRYASNS-----DNPVFVN-----DTGGANPIFQOI 615

US-09-173-891-43
Sequence 43, Application US/09173891
Patent No. 6077937
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meier, Henry
APPLICANT: Uick, Heidi Jane
APPLICANT: Foncerrada, Luis
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active

TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,232
FILING DATE:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: 86Q3
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 86Q3C
US-09-173-891-43

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Best Local Similarity 20.7%; Pred. No. 6.1;
Matches 74; Conservative 37; Mismatches 108; Indels 139; Gaps 18;

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QY 186 -----YSDNSTVYVFDNGTVFVQWDHVLQGWEDKG-----SF 219
DB 572 SIGIPITNVTKHNYQVRCRYASNS-----DNPVFVN-----DTGGANPIFQOI 615

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RESULT 12
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; Sequence 18, Application US/08484993B
; Patent No. 5837497
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,993B
; FILING DATE: 09-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-993B-18

Query Match 3.4%; Score 90.5; DB 2; Length 424;
Best Local Similarity 19.5%; Pred. No. 1.8;
Matches 86; Conservative 67; Mismatches 165; Indels 123; Gaps 22;

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QY 180 ANFNPGYSDNS-----TVVYFDNGTVFVQWHDVYLGQW-EDKGSFTFOAA-L 225
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QY 435 L-LVAAIILAGIYINGHPTS 453
Db 393 VLSLTLATIVLGLARRHHTAS 413

RESULT 13
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; Sequence 18, Application US/08484158B
; Patent No. 5976545
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; TITLE OF INVENTION: Pharmaceutical Compositions for
; IMMUNOCONTRACEPTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,158B
; FILING DATE: 07-JUNE-95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,223
; FILING DATE: 09-NOV-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 32794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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Wed Apr 23 07:41:52 2003

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223
; FILING DATE: 09-NOV-1993
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-150A-18

Query Match      3.4%; Score 90.5; DB 2; Length 424;
Best Local Similarity 19.5%; pred. No. 1.8;
Matches 86; Conservative 67; Mismatches 165; Indels 123; Gaps 22;

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QY 120 KHTILSNTHQASRVVLSDFEPFYGHPLRQITATGTFIFMGDVIHRMLTATQYVAPLM 179
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Search completed: April 22, 2003, 16:08:47
Job time : 26 secs

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251	6	1.2	527	4	US-09-134-001C-3358	Sequence 3358, Ap	324	6	1.2	650	4	US-09-232-200-79	Sequence 79, Appl
252	6	1.2	529	3	US-08-821-984-6	Sequence 6, Appli	325	6	1.2	650	4	US-09-232-200-97	Sequence 97, Appl
253	6	1.2	529	3	US-08-821-984-8	Sequence 8, Appli	326	6	1.2	650	4	US-09-232-197-79	Sequence 79, Appl
254	6	1.2	529	4	US-09-329-749-6	Sequence 6, Appli	327	6	1.2	650	4	US-09-232-197-97	Sequence 97, Appl
255	6	1.2	529	4	US-09-329-749-8	Sequence 8, Appli	328	6	1.2	650	4	US-09-232-201-79	Sequence 79, Appl
256	6	1.2	540	4	US-08-991-677-8	Sequence 8, Appli	329	6	1.2	650	4	US-09-232-201-97	Sequence 97, Appl
257	6	1.2	544	4	US-09-615-192A-349	Sequence 349, App	330	6	1.2	652	2	US-08-751-305-2	Sequence 2, Appli
258	6	1.2	546	1	US-08-487-990A-99	Sequence 99, Appl	331	6	1.2	654	1	US-08-441-139-11	Sequence 11, Appl
259	6	1.2	546	2	US-08-478-435-99	Sequence 99, Appl	332	6	1.2	655	4	US-09-632-538C-36	Sequence 36, Appl
260	6	1.2	546	2	US-08-337-483-99	Sequence 99, Appl	333	6	1.2	662	1	US-07-841-651-4	Sequence 4, Appli
261	6	1.2	546	2	US-08-478-373-99	Sequence 99, Appl	334	6	1.2	663	1	US-08-441-139-7	Sequence 7, Appli
262	6	1.2	546	3	US-08-474-671-99	Sequence 99, Appl	335	6	1.2	666	1	US-08-441-139-16	Sequence 16, Appl
263	6	1.2	546	3	US-08-483-577A-99	Sequence 99, Appl	336	6	1.2	668	1	US-09-930-181-2	Sequence 2, Appli
264	6	1.2	546	4	US-08-897-438-99	Sequence 99, Appl	337	6	1.2	670	1	US-08-363-208-2	Sequence 2, Appli
265	6	1.2	546	4	US-08-637-654-99	Sequence 99, Appl	338	6	1.2	670	4	US-09-137-478-2	Sequence 2, Appli
266	6	1.2	546	4	US-08-649-518-99	Sequence 99, Appl	339	6	1.2	671	2	US-08-426-125-8	Sequence 8, Appli
267	6	1.2	547	1	US-07-961-522-2	Sequence 2, Appli	340	6	1.2	671	2	US-08-455-353-8	Sequence 8, Appli
268	6	1.2	547	1	US-07-961-522-5	Sequence 5, Appli	341	6	1.2	679	1	US-08-214-583-2	Sequence 2, Appli
269	6	1.2	547	1	US-08-217-438-2	Sequence 2, Appli	342	6	1.2	682	1	US-08-441-139-5	Sequence 5, Appli
270	6	1.2	547	1	US-08-217-438-6	Sequence 6, Appli	343	6	1.2	685	3	US-08-872-855-2	Sequence 2, Appli
271	6	1.2	547	1	US-08-321-978-2	Sequence 2, Appli	344	6	1.2	700	4	US-07-757-342D-3	Sequence 3, Appli
272	6	1.2	547	1	US-08-321-978-5	Sequence 5, Appli	345	6	1.2	704	4	US-09-370-838-191	Sequence 191, App
273	6	1.2	547	2	US-08-710-584-2	Sequence 2, Appli	346	6	1.2	726	4	US-09-511-507-10	Sequence 10, Appl
274	6	1.2	547	2	US-08-710-584-5	Sequence 5, Appli	347	6	1.2	726	4	US-09-511-507-10	Sequence 10, Appl
275	6	1.2	549	4	US-09-134-001C-2973	Sequence 2973, Ap	348	6	1.2	731	2	US-08-911-364-1	Sequence 1, Appli
276	6	1.2	550	1	US-08-318-947A-4	Sequence 4, Appli	349	6	1.2	731	4	US-09-185-160-11	Sequence 11, Appl
277	6	1.2	550	2	US-08-795-303-4	Sequence 4, Appli	350	6	1.2	734	4	US-08-464-700-2	Sequence 2, Appli
278	6	1.2	551	4	US-09-194-145-2	Sequence 4, Appli	351	6	1.2	789	4	US-09-185-160-13	Sequence 13, Appl
279	6	1.2	551	6	5198359-2	Sequence 2, Appli	352	6	1.2	790	3	US-09-390-234-16	Sequence 16, Appl
280	6	1.2	551	6	549756-2	Patent No. 5198359	353	6	1.2	790	4	US-08-537-361E-8	Sequence 8, Appli
281	6	1.2	563	4	US-09-422-936-79	Sequence 79, Appl	354	6	1.2	790	4	US-08-817-707-6	Sequence 6, Appli
282	6	1.2	573	4	US-09-042-785A-2	Sequence 2, Appli	355	6	1.2	791	3	US-08-537-361E-4	Sequence 4, Appli
283	6	1.2	582	2	US-08-403-852D-20	Sequence 20, Appl	356	6	1.2	791	4	US-08-817-707-4	Sequence 4, Appli
284	6	1.2	582	3	US-08-510-646B-21	Sequence 21, Appl	357	6	1.2	792	1	US-08-326-670A-2	Sequence 2, Appli
285	6	1.2	582	4	US-09-231-818-20	Sequence 20, Appl	358	6	1.2	792	3	US-08-678-039A-40	Sequence 40, Appl
286	6	1.2	585	4	US-09-930-181-4	Sequence 4, Appli	359	6	1.2	792	3	US-08-537-361E-2	Sequence 2, Appli
287	6	1.2	591	3	US-08-996-139-2	Sequence 2, Appli	360	6	1.2	792	3	US-08-537-361E-6	Sequence 6, Appli
288	6	1.2	591	4	US-08-995-659-2	Sequence 2, Appli	361	6	1.2	792	3	US-08-990-470A-2	Sequence 2, Appli
289	6	1.2	591	4	US-09-215-649A-2	Sequence 2, Appli	362	6	1.2	795	4	US-08-817-707-2	Sequence 2, Appli
290	6	1.2	591	4	US-09-577-780-2	Sequence 2, Appli	363	6	1.2	796	2	US-07-741-453A-55	Sequence 55, Appl
291	6	1.2	593	1	US-07-961-522-4	Sequence 4, Appli	364	6	1.2	796	4	US-08-817-900-2	Sequence 2, Appli
292	6	1.2	593	1	US-08-217-438-4	Sequence 4, Appli	365	6	1.2	796	4	US-08-868-699A-2	Sequence 2, Appli
293	6	1.2	593	1	US-08-217-438-5	Sequence 5, Appli	366	6	1.2	796	4	US-09-236-645-2	Sequence 2, Appli
294	6	1.2	593	1	US-08-487-890A-100	Sequence 100, App	367	6	1.2	801	4	US-09-757-014-2	Sequence 2, Appli
295	6	1.2	593	1	US-08-321-978-4	Sequence 4, Appli	368	6	1.2	811	4	US-09-104-070-2	Sequence 2, Appli
296	6	1.2	593	2	US-08-710-584-4	Sequence 4, Appli	369	6	1.2	819	4	US-09-199-637A-93	Sequence 93, Appl
297	6	1.2	593	2	US-08-478-435-100	Sequence 100, App	370	6	1.2	819	4	US-09-651-656-15	Sequence 15, Appl
298	6	1.2	593	2	US-08-337-483-100	Sequence 100, App	371	6	1.2	819	4	US-09-650-855-15	Sequence 15, Appl
299	6	1.2	593	2	US-08-478-373-100	Sequence 100, App	372	6	1.2	839	4	US-09-197-636-2	Sequence 2, Appli
300	6	1.2	593	3	US-08-474-671-100	Sequence 100, App	373	6	1.2	839	4	US-09-197-636-4	Sequence 4, Appli
301	6	1.2	593	3	US-08-483-577A-100	Sequence 100, App	374	6	1.2	839	4	US-09-197-636-8	Sequence 8, Appli
302	6	1.2	593	4	US-08-897-438-100	Sequence 100, App	375	6	1.2	839	4	US-09-235-451-34	Sequence 34, Appl
303	6	1.2	593	4	US-08-637-654-100	Sequence 100, App	376	6	1.2	844	4	US-09-533-220A-2	Sequence 2, Appli
304	6	1.2	593	4	US-08-649-518-100	Sequence 100, App	377	6	1.2	844	4	US-09-422-936-47	Sequence 47, Appl
305	6	1.2	596	2	US-08-836-620A-16	Sequence 16, Appl	378	6	1.2	848	4	US-09-422-936-51	Sequence 51, Appl
306	6	1.2	600	6	5240706-1	Patent No. 5240706	379	6	1.2	864	4	US-08-976-255-10	Sequence 10, Appl
307	6	1.2	603	4	US-09-930-181-17	Sequence 17, Appl	380	6	1.2	864	4	US-09-604-978-11	Sequence 11, Appl
308	6	1.2	607	2	US-08-472-534-5	Sequence 5, Appli	381	6	1.2	877	1	US-08-072-574-12	Sequence 12, Appl
309	6	1.2	608	4	US-09-130-491-13	Sequence 13, Appl	382	6	1.2	877	3	US-08-486-270-12	Sequence 12, Appl
310	6	1.2	612	3	US-09-295-186-16	Sequence 16, Appl	383	6	1.2	877	3	US-08-367-264-12	Sequence 12, Appl
311	6	1.2	616	3	US-08-996-139-6	Sequence 6, Appli	384	6	1.2	877	4	US-09-153-757-12	Sequence 12, Appl
312	6	1.2	616	4	US-08-995-659-6	Sequence 6, Appli	385	6	1.2	886	4	US-09-422-936-77	Sequence 77, Appl
313	6	1.2	616	4	US-09-215-649A-6	Sequence 6, Appli	386	6	1.2	890	4	US-09-513-783A-174	Sequence 174, App
314	6	1.2	616	4	US-09-134-001C-3646	Sequence 3646, Ap	387	6	1.2	892	4	US-09-422-936-75	Sequence 75, Appl
315	6	1.2	616	4	US-09-577-780-6	Sequence 6, Appli	388	6	1.2	899	4	US-09-422-936-71	Sequence 71, Appl
316	6	1.2	641	1	US-08-441-139-4	Sequence 4, Appli	389	6	1.2				
317	6	1.2	641	2	US-08-873-479-42	Sequence 42, Appli	390	6	1.2				
318	6	1.2	644	4	US-08-797-358B-3	Sequence 3, Appli	391	6	1.2				
319	6	1.2	644	4	US-09-300-909-18	Sequence 18, Appl	392	6	1.2				

393	6	1.2	905	1	US-08-072-574-2	Sequence 2, Appli	Sequence 2, Appli	466	6	1.2	1581	4	US-09-208-716-4	Sequence 4, Appli
394	6	1.2	906	1	US-08-486-270-2	Sequence 2, Appli	Sequence 2, Appli	467	6	1.2	1582	2	US-08-404-531B-9	Sequence 9, Appli
395	6	1.2	906	3	US-08-367-264-2	Sequence 2, Appli	Sequence 2, Appli	468	6	1.2	1582	3	US-08-476-900A-9	Sequence 9, Appli
396	6	1.2	906	4	US-09-153-757-2	Sequence 2, Appli	Sequence 2, Appli	469	6	1.2	1582	3	US-08-488-546A-9	Sequence 9, Appli
397	6	1.2	906	5	PCT-US91-09422-17	Sequence 17, Appl	Sequence 17, Appl	470	6	1.2	1582	4	US-08-726-320-5	Sequence 5, Appli
398	6	1.2	914	4	US-09-134-001C-5208	Sequence 5208, Ap	Sequence 5208, Ap	471	6	1.2	1582	4	US-08-208-716-5	Sequence 5, Appli
399	6	1.2	935	1	US-08-006-676B-1	Sequence 1, Appli	Sequence 1, Appli	472	6	1.2	1651	1	US-08-447-411-2	Sequence 2, Appli
400	6	1.2	955	1	US-08-282-845-2	Sequence 2, Appli	Sequence 2, Appli	473	6	1.2	1745	2	US-09-031-485-33	Sequence 33, Appl
401	6	1.2	955	2	US-08-428-414A-3	Sequence 3, Appli	Sequence 3, Appli	474	6	1.2	1745	3	US-08-847-429A-33	Sequence 33, Appl
402	6	1.2	955	5	PCT-US94-00324-1	Sequence 1, Appli	Sequence 1, Appli	475	6	1.2	1745	3	US-09-065-474-33	Sequence 33, Appl
403	6	1.2	960	4	US-09-422-936-45	Sequence 45, Appl	Sequence 45, Appl	476	6	1.2	1745	4	US-09-557-034-33	Sequence 33, Appl
404	6	1.2	961	4	US-09-422-936-49	Sequence 49, Appl	Sequence 49, Appl	477	6	1.2	2343	4	US-09-324-867-2	Sequence 2, Appli
405	6	1.2	964	4	US-09-422-936-53	Sequence 53, Appl	Sequence 53, Appl	478	6	1.2	2532	4	US-09-215-694-10	Sequence 10, Appl
406	6	1.2	967	4	US-09-130-491-2	Sequence 2, Appli	Sequence 2, Appli	479	6	1.2	2549	4	US-08-471-112A-3	Sequence 3, Appli
407	6	1.2	984	4	US-09-287-354-2	Sequence 2, Appli	Sequence 2, Appli	480	6	1.2	2549	5	PCT-US95-06722-12	Sequence 12, Appli
408	6	1.2	1005	4	US-09-770-170-4	Sequence 4, Appli	Sequence 4, Appli	481	6	1.2	2890	6	5206163-3	Patent No. 5206163
409	6	1.2	1038	4	US-08-334-179A-2	Sequence 2, Appli	Sequence 2, Appli	482	6	1.2	2890	4	US-09-413-814-67	Sequence 67, Appl
410	6	1.2	1038	4	US-08-334-179A-8	Sequence 8, Appli	Sequence 8, Appli	483	6	1.2	3025	6	523423-3	Patent No. 523423
411	6	1.2	1056	2	US-08-687-289A-7	Sequence 7, Appli	Sequence 7, Appli	484	6	1.2	3031	1	US-07-689-008-2	Sequence 2, Appli
412	6	1.2	1056	2	US-08-687-289A-8	Sequence 8, Appli	Sequence 8, Appli	485	6	1.2	3461	4	US-09-334-220-2	Sequence 2, Appli
413	6	1.2	1075	2	US-08-993-228-19	Sequence 19, Appl	Sequence 19, Appl	486	6	1.2	3798	3	US-09-335-409-6	Sequence 6, Appli
414	6	1.2	1075	3	US-08-545-860D-55	Sequence 55, Appl	Sequence 55, Appl	487	6	1.2	3798	4	US-09-568-102-6	Sequence 6, Appli
415	6	1.2	1093	5	PCT-US94-04496-55	Sequence 55, Appl	Sequence 55, Appl	488	6	1.2	3798	4	US-09-567-969-6	Sequence 6, Appli
416	6	1.2	1142	4	US-09-106-075A-89	Sequence 89, Appl	Sequence 89, Appl	489	6	1.2	3798	4	US-09-568-480-6	Sequence 6, Appli
417	6	1.2	1147	1	US-08-131-365B-38	Sequence 38, Appl	Sequence 38, Appl	490	6	1.2	3798	4	US-09-568-486-6	Sequence 6, Appli
418	6	1.2	1147	2	US-08-668-123-38	Sequence 38, Appl	Sequence 38, Appl	491	6	1.2	3798	4	US-09-568-472-6	Sequence 6, Appli
419	6	1.2	1180	1	US-08-072-574-8	Sequence 8, Appli	Sequence 8, Appli	492	6	1.2	3798	4	US-09-567-899-6	Sequence 6, Appli
420	6	1.2	1180	3	US-08-367-264-8	Sequence 8, Appli	Sequence 8, Appli	493	6	1.2	4551	3	US-09-320-878-1	Sequence 1, Appli
421	6	1.2	1180	3	US-08-367-264-8	Sequence 8, Appli	Sequence 8, Appli	494	6	1.2	4613	4	US-09-105-537-31	Sequence 31, Appl
422	6	1.2	1180	4	US-08-660-148-2	Sequence 2, Appli	Sequence 2, Appli	495	6	1.2	7257	3	US-09-335-409-5	Sequence 5, Appli
423	6	1.2	1180	4	US-09-153-757-8	Sequence 8, Appli	Sequence 8, Appli	496	6	1.2	7257	4	US-09-568-102-5	Sequence 5, Appli
424	6	1.2	1186	1	US-08-485-568A-4	Sequence 4, Appli	Sequence 4, Appli	497	6	1.2	7257	4	US-09-567-969-5	Sequence 5, Appli
425	6	1.2	1186	1	US-08-357-698-6	Sequence 6, Appli	Sequence 6, Appli	498	6	1.2	7257	4	US-09-568-480-5	Sequence 5, Appli
426	6	1.2	1186	2	US-08-590-554A-4	Sequence 4, Appli	Sequence 4, Appli	499	6	1.2	7257	4	US-09-568-486-5	Sequence 5, Appli
427	6	1.2	1186	2	US-09-184-223-4	Sequence 4, Appli	Sequence 4, Appli	500	6	1.2	7257	4	US-09-568-472-5	Sequence 5, Appli
428	6	1.2	1186	5	PCT-US93-12682-6	Sequence 6, Appli	Sequence 6, Appli	501	6	1.2	7257	4	US-09-567-899-5	Sequence 5, Appli
429	6	1.2	1189	4	US-09-287-354-3	Sequence 3, Appli	Sequence 3, Appli	502	6	1.2	11877	4	US-09-105-537-6	Sequence 6, Appli
430	6	1.2	1189	4	US-09-287-354-4	Sequence 4, Appli	Sequence 4, Appli	503	5	1.0	5	2	US-08-679-865-21	Sequence 21, Appl
431	6	1.2	1194	4	US-08-538-526-1	Sequence 1, Appli	Sequence 1, Appli	504	5	1.0	5	2	US-08-680-876-21	Sequence 21, Appl
432	6	1.2	1199	1	US-08-041-538-2	Sequence 2, Appli	Sequence 2, Appli	505	5	1.0	5	4	US-08-974-549A-173	Sequence 173, App
433	6	1.2	1199	1	US-08-463-642-2	Sequence 2, Appli	Sequence 2, Appli	506	5	1.0	5	4	US-09-263-975-21	Sequence 21, Appl
434	6	1.2	1199	1	US-08-455-602-2	Sequence 2, Appli	Sequence 2, Appli	507	5	1.0	5	4	US-08-665-643A-48	Sequence 48, Appl
435	6	1.2	1199	2	US-08-465-157-2	Sequence 2, Appli	Sequence 2, Appli	508	5	1.0	5	4	US-08-665-643A-49	Sequence 49, Appl
436	6	1.2	1199	5	PCT-US91-09422-2	Sequence 2, Appli	Sequence 2, Appli	509	5	1.0	5	4	US-09-187-859-1905	Sequence 1905, Ap
437	6	1.2	1212	1	US-08-072-574-10	Sequence 10, Appl	Sequence 10, Appl	510	5	1.0	6	1	US-08-287-717-14	Sequence 14, Appl
438	6	1.2	1212	1	US-08-486-270-10	Sequence 10, Appl	Sequence 10, Appl	511	5	1.0	6	1	US-08-441-914-14	Sequence 14, Appl
439	6	1.2	1212	3	US-08-367-264-10	Sequence 10, Appl	Sequence 10, Appl	512	6	1.0	6	2	US-08-340-283-162	Sequence 162, App
440	6	1.2	1212	4	US-08-660-148-5	Sequence 5, Appli	Sequence 5, Appli	513	5	1.0	6	4	US-09-608-790-5	Sequence 5, Appli
441	6	1.2	1212	4	US-09-153-757-10	Sequence 6, Appli	Sequence 6, Appli	514	5	1.0	6	4	US-09-608-790-6	Sequence 6, Appli
442	6	1.2	1219	2	US-08-687-289A-6	Sequence 6, Appli	Sequence 6, Appli	515	5	1.0	7	1	US-08-213-124-3	Sequence 3, Appli
443	6	1.2	1220	2	US-08-843-530B-36	Sequence 36, Appl	Sequence 36, Appl	516	5	1.0	7	3	US-08-485-324-1	Sequence 1, Appli
444	6	1.2	1227	2	US-08-760-075A-18	Sequence 18, Appl	Sequence 18, Appl	517	5	1.0	7	3	US-08-485-324-17	Sequence 17, Appl
445	6	1.2	1227	4	US-09-338-546-18	Sequence 18, Appl	Sequence 18, Appl	518	5	1.0	7	3	US-08-447-506-1	Sequence 1, Appli
446	6	1.2	1227	4	US-09-659-084-18	Sequence 18, Appl	Sequence 18, Appl	519	5	1.0	7	3	US-08-447-506-17	Sequence 17, Appl
447	6	1.2	1257	4	US-09-220-641-3	Sequence 3, Appli	Sequence 3, Appli	520	5	1.0	7	3	US-08-235-437-1	Sequence 1, Appli
448	6	1.2	1317	3	US-09-083-521-7	Sequence 7, Appli	Sequence 7, Appli	521	5	1.0	7	3	US-08-235-437-17	Sequence 17, Appl
449	6	1.2	1326	4	US-09-147-236-5	Sequence 5, Appli	Sequence 5, Appli	522	5	1.0	7	4	US-09-173-941-102	Sequence 102, App
450	6	1.2	1422	4	US-08-469-260A-85	Sequence 85, Appl	Sequence 85, Appl	523	5	1.0	7	4	US-08-447-515-1	Sequence 1, Appli
451	6	1.2	1498	2	US-08-404-531B-28	Sequence 28, Appl	Sequence 28, Appl	524	5	1.0	7	4	US-08-447-515-17	Sequence 17, Appl
452	6	1.2	1498	2	US-08-404-531B-29	Sequence 29, Appl	Sequence 29, Appl	525	5	1.0	7	4	US-08-469-260A-497	Sequence 497, App
453	6	1.2	1498	3	US-08-476-900A-28	Sequence 28, Appl	Sequence 28, Appl	526	5	1.0	8	2	US-08-679-865-31	Sequence 31, Appl
454	6	1.2	1498	3	US-08-476-900A-29	Sequence 29, Appl	Sequence 29, Appl	527	5	1.0	8	2	US-08-679-865-32	Sequence 32, Appl
455	6	1.2	1498	3	US-08-488-546A-28	Sequence 28, Appl	Sequence 28, Appl	528	5	1.0	8	2	US-08-680-876-31	Sequence 31, Appl
456	6	1.2	1498	3	US-08-488-546A-29	Sequence 29, Appl	Sequence 29, Appl	529	5	1.0	8	2	US-08-680-876-32	Sequence 32, Appl
457	6	1.2	1536	4	US-09-413-814-10	Sequence 10, Appl	Sequence 10, Appl	530	5	1.0	8	4	US-09-263-975-31	Sequence 31, Appl
458	6	1.2	1580	4	US-08-726-320-1	Sequence 1, Appli	Sequence 1, Appli	531	5	1.0	8	4	US-09-263-975-32	Sequence 32, Appl
459	6	1.2	1580	4	US-09-208-716-1	Sequence 1, Appli	Sequence 1, Appli	532	5	1.0	8	4	US-08-988-842-41	Sequence 41, Appl
460	6	1.2	1581	2	US-08-404-531B-6	Sequence 6, Appli	Sequence 6, Appli	533	5	1.0	9	1	US-08-465-167A-34	Sequence 34, Appl
461	6	1.2	1581	3	US-08-476-900A-6	Sequence 6, Appli	Sequence 6, Appli	534	5	1.0	9	2	US-08-640-765A-7	Sequence 7, Appli
462	6	1.2	1581	3	US-08-488-546A-6	Sequence 6, Appli	Sequence 6, Appli	535	5	1.0	9	2	US-08-340-283-30	Sequence 30, Appl
463	6	1.2	1581	4	US-08-726-320-3	Sequence 3, Appli	Sequence 3, Appli	536	5	1.0	9	2	US-08-340-283-92	Sequence 92, Appl
464	6	1.2	1581	4	US-08-726-320-4	Sequence 4, Appli	Sequence 4, Appli	537	5	1.0	9	2	US-08-340-283-114	Sequence 114, App
465	6	1.2	1581	4	US-09-208-716-3	Sequence 3, Appli	Sequence 3, Appli	538	5	1.0	9	2	US-08-679-865-33	Sequence 33, Appl

539	5	1.0	9	2	US-08-680-876-33	Sequence 33, Appl	612	5	1.0	15	2	US-08-599-654-51	Sequence 51, Appl
540	5	1.0	9	2	US-08-986-234-97	Sequence 97, Appl	613	5	1.0	15	3	US-08-944-868A-51	Sequence 51, Appl
541	5	1.0	9	4	US-09-073-613-7	Sequence 7, Appl	614	5	1.0	15	3	US-08-944-423A-51	Sequence 51, Appl
542	5	1.0	9	4	US-09-263-975-33	Sequence 33, Appl	615	5	1.0	15	3	US-08-466-680B-44	Sequence 44, Appl
543	5	1.0	9	4	US-09-306-542A-39	Sequence 39, Appl	616	5	1.0	15	3	US-08-944-496-51	Sequence 51, Appl
544	5	1.0	9	4	US-09-257-179-112	Sequence 112, App	617	5	1.0	15	4	US-09-230-222-24	Sequence 24, Appl
545	5	1.0	9	4	US-09-359-304B-2	Sequence 2, Appl	618	5	1.0	15	4	US-08-602-999A-366	Sequence 366, App
546	5	1.0	9	4	US-09-359-304B-5	Sequence 5, Appl	619	5	1.0	15	4	US-09-026-904-15	Sequence 15, Appl
547	5	1.0	9	4	US-09-359-304B-7	Sequence 7, Appl	620	5	1.0	15	4	US-09-336-447A-33	Sequence 33, Appl
548	5	1.0	10	1	US-08-075-533-7	Sequence 7, Appl	621	5	1.0	15	4	US-09-009-953-41	Sequence 41, Appl
549	5	1.0	10	1	US-08-465-167A-51	Sequence 51, Appl	622	5	1.0	15	4	US-09-009-953-45	Sequence 45, Appl
550	5	1.0	10	2	US-08-679-865-12	Sequence 12, Appl	623	5	1.0	15	4	US-09-009-953-47	Sequence 47, Appl
551	5	1.0	10	2	US-08-679-865-34	Sequence 34, Appl	624	5	1.0	15	4	US-09-009-953-52	Sequence 52, Appl
552	5	1.0	10	2	US-08-680-876-12	Sequence 12, Appl	625	5	1.0	15	4	US-09-500-124-366	Sequence 366, App
553	5	1.0	10	2	US-08-680-876-34	Sequence 34, Appl	626	5	1.0	15	6	5175148-2	Patent No. 5175148
554	5	1.0	10	2	US-08-948-176-7	Sequence 7, Appl	627	5	1.0	16	3	US-08-912-272-39	Sequence 39, Appl
555	5	1.0	10	3	US-08-159-339A-1038	Sequence 1038, Ap	628	5	1.0	16	4	US-09-323-433A-29	Sequence 29, Appl
556	5	1.0	10	4	US-09-263-975-12	Sequence 12, Appl	629	5	1.0	16	4	US-09-026-039-39	Sequence 39, Appl
557	5	1.0	10	4	US-09-263-975-34	Sequence 34, Appl	630	5	1.0	16	4	US-09-230-225B-7	Sequence 7, Appl
558	5	1.0	10	4	US-09-336-447A-34	Sequence 34, Appl	631	5	1.0	17	2	US-08-319-866-24	Sequence 24, Appl
559	5	1.0	10	5	PCT-US91-09160-7	Sequence 7, Appl	632	5	1.0	17	4	US-09-025-769B-243	Sequence 243, App
560	5	1.0	11	1	US-07-666-719-20	Sequence 20, Appl	633	5	1.0	17	4	US-09-265-653-19	Sequence 19, Appl
561	5	1.0	11	2	US-08-679-865-35	Sequence 35, Appl	634	5	1.0	18	1	US-07-666-719-12	Sequence 12, Appl
562	5	1.0	11	2	US-08-680-876-35	Sequence 35, Appl	635	5	1.0	18	1	US-08-612-302A-42	Sequence 42, Appl
563	5	1.0	11	4	US-09-263-975-35	Sequence 35, Appl	636	5	1.0	18	2	US-08-240-514-42	Sequence 42, Appl
564	5	1.0	12	2	US-08-406-330-80	Sequence 80, Appl	637	5	1.0	18	2	US-09-017-205-41	Sequence 41, Appl
565	5	1.0	12	2	US-08-347-335A-11	Sequence 11, Appl	638	5	1.0	18	2	US-09-017-205-42	Sequence 42, Appl
566	5	1.0	12	2	US-08-556-597-80	Sequence 80, Appl	639	5	1.0	18	3	US-08-912-272-7	Sequence 7, Appl
567	5	1.0	12	3	US-08-599-226-27	Sequence 27, Appl	640	5	1.0	18	3	US-08-912-272-38	Sequence 38, Appl
568	5	1.0	12	3	US-08-599-226-28	Sequence 28, Appl	641	5	1.0	18	3	US-08-912-272-40	Sequence 40, Appl
569	5	1.0	12	3	US-08-599-226-29	Sequence 29, Appl	642	5	1.0	18	4	US-09-157-910-2	Sequence 2, Appl
570	5	1.0	12	3	US-08-599-226-30	Sequence 30, Appl	643	5	1.0	18	4	US-09-026-039-7	Sequence 7, Appl
571	5	1.0	12	3	US-08-599-226-32	Sequence 32, Appl	644	5	1.0	18	4	US-09-026-039-38	Sequence 38, Appl
572	5	1.0	12	3	US-08-599-226-33	Sequence 33, Appl	645	5	1.0	18	4	US-09-026-039-40	Sequence 40, Appl
573	5	1.0	12	4	US-09-125-098-27	Sequence 27, Appl	646	5	1.0	18	4	US-09-082-358B-16	Sequence 16, Appl
574	5	1.0	12	4	US-09-125-098-28	Sequence 28, Appl	647	5	1.0	19	3	US-08-943-173-12	Sequence 12, Appl
575	5	1.0	12	4	US-09-125-098-29	Sequence 29, Appl	648	5	1.0	19	4	US-09-345-468-8	Sequence 8, Appl
576	5	1.0	12	4	US-09-125-098-30	Sequence 30, Appl	649	5	1.0	19	4	US-08-957-130-20	Sequence 20, Appl
577	5	1.0	12	4	US-09-125-098-32	Sequence 32, Appl	650	5	1.0	19	4	US-09-414-453A-8	Sequence 8, Appl
578	5	1.0	12	4	US-09-125-098-33	Sequence 33, Appl	651	5	1.0	19	4	US-08-918-428D-16	Sequence 16, Appl
579	5	1.0	12	4	US-09-025-769B-191	Sequence 191, App	652	5	1.0	20	1	US-07-651-710A-21	Sequence 21, Appl
580	5	1.0	13	1	US-08-075-533-5	Sequence 5, Appl	653	5	1.0	20	1	US-07-798-776-13	Sequence 13, Appl
581	5	1.0	13	2	US-08-292-968-34	Sequence 34, Appl	654	5	1.0	20	1	US-07-798-776-21	Sequence 21, Appl
582	5	1.0	13	2	US-08-679-865-13	Sequence 13, Appl	655	5	1.0	20	1	US-08-218-025A-27	Sequence 27, Appl
583	5	1.0	13	2	US-08-680-876-13	Sequence 13, Appl	656	5	1.0	20	1	US-07-678-974D-8	Sequence 8, Appl
584	5	1.0	13	2	US-08-948-176-5	Sequence 5, Appl	657	5	1.0	20	2	US-08-140-137A-38	Sequence 38, Appl
585	5	1.0	13	2	US-08-467-974-34	Sequence 34, Appl	658	5	1.0	20	2	US-08-934-915-151	Sequence 151, App
586	5	1.0	13	2	US-08-467-976-34	Sequence 34, Appl	659	5	1.0	20	2	US-08-945-168-13	Sequence 13, Appl
587	5	1.0	13	3	US-08-467-976-34	Sequence 34, Appl	660	5	1.0	20	3	US-08-251-288A-13	Sequence 13, Appl
588	5	1.0	13	3	US-08-526-136-21	Sequence 21, Appl	661	5	1.0	20	3	US-08-251-288A-21	Sequence 21, Appl
589	5	1.0	13	4	US-09-082-514-34	Sequence 34, Appl	662	5	1.0	20	3	US-09-298-819A-13	Sequence 13, Appl
590	5	1.0	13	4	US-09-263-975-13	Sequence 13, Appl	663	5	1.0	20	3	US-09-298-819A-21	Sequence 21, Appl
591	5	1.0	13	4	US-08-817-787-7	Sequence 7, Appl	664	5	1.0	20	4	US-09-333-373-1	Sequence 1, Appl
592	5	1.0	13	5	PCT-US91-09160-5	Sequence 5, Appl	665	5	1.0	20	4	US-09-586-563C-13	Sequence 13, Appl
593	5	1.0	13	5	PCT-US95-04121-47	Sequence 47, Appl	666	5	1.0	20	4	US-09-586-563C-21	Sequence 21, Appl
594	5	1.0	14	1	US-08-321-668-24	Sequence 24, Appl	667	5	1.0	20	4	US-09-586-562C-13	Sequence 13, Appl
595	5	1.0	14	1	US-08-837-941-24	Sequence 24, Appl	668	5	1.0	20	4	US-09-586-562C-21	Sequence 21, Appl
596	5	1.0	14	2	US-08-637-759B-153	Sequence 153, App	669	5	1.0	20	6	5427917-1	Patent No. 5427917
597	5	1.0	14	2	US-07-876-941A-23	Sequence 23, Appl	670	5	1.0	21	1	US-07-868-353A-4	Sequence 4, Appl
598	5	1.0	14	3	US-08-871-355A-153	Sequence 153, App	671	5	1.0	21	2	US-08-407-804-4	Sequence 4, Appl
599	5	1.0	14	4	US-09-217-228-17	Sequence 17, Appl	672	5	1.0	21	2	US-08-712-212-2	Sequence 2, Appl
600	5	1.0	14	4	US-09-217-228-18	Sequence 18, Appl	673	5	1.0	21	2	US-08-894-339-8	Sequence 8, Appl
601	5	1.0	14	4	US-09-201-945-153	Sequence 153, App	674	5	1.0	21	3	US-09-124-807-4	Sequence 4, Appl
602	5	1.0	14	4	US-09-400-653A-42	Sequence 42, Appl	675	5	1.0	21	4	US-09-306-044-8	Sequence 8, Appl
603	5	1.0	15	1	US-08-030-731A-27	Sequence 27, Appl	676	5	1.0	21	4	US-09-286-959B-23	Sequence 23, Appl
604	5	1.0	15	1	US-07-854-603-14	Sequence 14, Appl	677	5	1.0	21	4	US-09-106-568E-117	Sequence 117, App
605	5	1.0	15	1	US-08-467-083-44	Sequence 44, Appl	678	5	1.0	21	5	PCT-US95-05160-2	Sequence 2, Appl
606	5	1.0	15	1	US-08-414-417B-44	Sequence 44, Appl	679	5	1.0	22	2	US-08-140-137A-24	Sequence 24, Appl
607	5	1.0	15	2	US-08-140-137A-32	Sequence 32, Appl	680	5	1.0	22	2	US-08-637-759B-114	Sequence 114, App
608	5	1.0	15	2	US-08-486-348A-44	Sequence 44, Appl	681	5	1.0	22	2	US-08-902-516-6	Sequence 6, Appl
609	5	1.0	15	2	US-08-616-844-51	Sequence 51, Appl	682	5	1.0	22	3	US-08-871-355A-114	Sequence 114, App
610	5	1.0	15	2	US-08-687-956A-9	Sequence 9, Appl	683	5	1.0	22	4	US-09-201-945-114	Sequence 114, App
611	5	1.0	15	2	US-08-468-545B-44	Sequence 44, Appl	684	5	1.0	22	4	US-09-106-568E-29	Sequence 29, Appl

685	5	1.0	22	4	US-09-106-568E-69	Sequence 69, Appl	758	5	1.0	29	4	US-09-699-684-12	Sequence 12, Appl
686	5	1.0	22	6	526328-12	Patent No. 526328	759	5	1.0	29	4	US-09-699-684-20	Sequence 20, Appl
687	5	1.0	23	1	US-07-908-317-11	Sequence 11, Appl	760	5	1.0	29	6	5204096-34	Patent No. 5204096
688	5	1.0	23	1	US-08-264-093-23	Sequence 23, Appl	761	5	1.0	30	1	US-08-084-741A-5	Sequence 5, Appl
689	5	1.0	23	1	US-08-112-208C-17	Sequence 17, Appl	762	5	1.0	30	1	US-08-184-252A-7	Sequence 7, Appl
690	5	1.0	23	1	US-08-248-819A-19	Sequence 19, Appl	763	5	1.0	30	2	US-08-140-137A-41	Sequence 41, Appl
691	5	1.0	23	2	US-08-630-822A-75	Sequence 75, Appl	764	5	1.0	30	2	US-08-318-157B-30	Sequence 30, Appl
692	5	1.0	23	2	US-08-337-646A-37	Sequence 37, Appl	765	5	1.0	30	2	US-08-318-157B-32	Sequence 32, Appl
693	5	1.0	23	2	US-09-005-069-75	Sequence 75, Appl	766	5	1.0	30	4	US-09-348-578-5	Sequence 5, Appl
694	5	1.0	23	2	US-08-856-531-17	Sequence 17, Appl	767	5	1.0	30	4	US-09-348-578-13	Sequence 13, Appl
695	5	1.0	23	2	US-08-856-034-17	Sequence 17, Appl	768	5	1.0	30	4	US-09-348-578-21	Sequence 21, Appl
696	5	1.0	23	4	US-08-827-326-23	Sequence 23, Appl	769	5	1.0	30	4	US-09-699-684-5	Sequence 5, Appl
697	5	1.0	23	4	US-08-927-326-37	Sequence 37, Appl	770	5	1.0	30	4	US-09-699-684-13	Sequence 13, Appl
698	5	1.0	23	4	US-09-171-156A-4	Sequence 4, Appl	771	5	1.0	30	4	US-09-699-684-21	Sequence 21, Appl
699	5	1.0	23	4	US-09-186-276B-8	Sequence 8, Appl	772	5	1.0	30	5	PCT-US95-00601-7	Sequence 7, Appl
700	5	1.0	23	4	US-09-186-276B-8	Sequence 8, Appl	773	5	1.0	30	6	5464764-1	Patent No. 5464764
701	5	1.0	23	4	US-09-149-476-328	Sequence 328, App	774	5	1.0	31	1	US-08-190-802A-239	Sequence 239, App
702	5	1.0	23	4	US-08-842-445-5	Sequence 5, Appl	775	5	1.0	31	3	US-07-401-432-31	Sequence 31, Appl
703	5	1.0	23	4	US-08-842-445-5	Sequence 5, Appl	776	5	1.0	31	3	US-07-401-432-32	Sequence 32, Appl
704	5	1.0	23	4	US-09-186-188B-5	Sequence 5, Appl	777	5	1.0	31	4	US-09-348-578-6	Sequence 6, Appl
705	5	1.0	23	4	US-09-186-188B-8	Sequence 8, Appl	778	5	1.0	31	4	US-09-348-578-14	Sequence 14, Appl
706	5	1.0	23	4	PCT-US93-06171-11	Sequence 11, Appl	779	5	1.0	31	4	US-09-348-578-22	Sequence 22, Appl
707	5	1.0	23	5	PCT-US93-06171-11	Sequence 11, Appl	780	5	1.0	31	4	US-08-477-346-239	Sequence 239, App
708	5	1.0	24	1	US-07-794-288D-189	Sequence 189, App	781	5	1.0	31	4	US-08-473-089-239	Sequence 239, App
709	5	1.0	24	2	US-08-140-137A-37	Sequence 37, Appl	782	5	1.0	31	4	US-08-487-072A-239	Sequence 239, App
710	5	1.0	24	2	US-08-347-335A-19	Sequence 19, Appl	783	5	1.0	31	4	US-09-699-684-6	Sequence 6, Appl
711	5	1.0	24	2	US-09-000-041A-13	Sequence 13, Appl	784	5	1.0	31	4	US-09-699-684-14	Sequence 14, Appl
712	5	1.0	24	5	PCT-US92-07865-16	Sequence 16, Appl	785	5	1.0	31	4	US-09-699-684-22	Sequence 22, Appl
713	5	1.0	25	1	US-07-794-288D-181	Sequence 181, App	786	5	1.0	31	6	5245013-18	Patent No. 5245013
714	5	1.0	25	2	US-08-337-646A-29	Sequence 29, Appl	787	5	1.0	32	1	US-07-995-503A-5	Sequence 5, Appl
715	5	1.0	25	2	US-08-726-306A-67	Sequence 67, Appl	788	5	1.0	32	1	US-08-390-510-5	Sequence 5, Appl
716	5	1.0	25	4	US-08-927-326-29	Sequence 29, Appl	789	5	1.0	32	1	US-08-390-510-5	Sequence 5, Appl
717	5	1.0	25	4	US-09-336-536-52	Sequence 52, Appl	790	5	1.0	32	2	US-08-140-137A-27	Sequence 27, Appl
718	5	1.0	25	4	US-09-149-476-369	Sequence 369, App	791	5	1.0	32	2	US-08-390-509-5	Sequence 5, Appl
719	5	1.0	25	4	US-08-469-260A-180	Sequence 180, App	792	5	1.0	32	2	US-08-526-583-14	Sequence 14, Appl
720	5	1.0	26	4	US-08-918-428D-13	Sequence 13, Appl	793	5	1.0	32	2	US-08-595-868C-39	Sequence 39, Appl
721	5	1.0	26	4	US-09-082-358B-83	Sequence 83, Appl	794	5	1.0	32	2	US-08-595-868C-40	Sequence 40, Appl
722	5	1.0	27	1	US-08-140-188-13	Sequence 13, Appl	795	5	1.0	32	4	US-09-348-578-7	Sequence 7, Appl
723	5	1.0	27	1	US-08-481-888A-2	Sequence 2, Appl	796	5	1.0	32	4	US-09-348-578-15	Sequence 15, Appl
724	5	1.0	27	1	US-08-485-273A-2	Sequence 2, Appl	797	5	1.0	32	4	US-09-348-578-23	Sequence 23, Appl
725	5	1.0	27	2	US-08-522-229B-3	Sequence 3, Appl	798	5	1.0	32	4	US-09-149-860A-5	Sequence 5, Appl
726	5	1.0	27	2	US-08-169-948B-22	Sequence 22, Appl	799	5	1.0	32	4	US-09-139-819A-39	Sequence 39, Appl
727	5	1.0	27	2	US-08-448-873-22	Sequence 22, Appl	800	5	1.0	32	4	US-09-139-819A-40	Sequence 40, Appl
728	5	1.0	27	2	US-09-102-433-3	Sequence 3, Appl	801	5	1.0	32	4	US-09-227-357-181	Sequence 181, App
729	5	1.0	27	2	US-08-973-563A-2	Sequence 2, Appl	802	5	1.0	32	4	US-08-936-165A-459	Sequence 459, App
730	5	1.0	27	2	US-08-973-559-2	Sequence 2, Appl	803	5	1.0	32	4	US-09-750-913-39	Sequence 39, App
731	5	1.0	27	3	US-08-526-521-13	Sequence 13, Appl	804	5	1.0	32	4	US-09-750-913-40	Sequence 40, Appl
732	5	1.0	27	3	US-08-749-816-19	Sequence 19, Appl	805	5	1.0	32	4	US-09-699-684-7	Sequence 7, Appl
733	5	1.0	27	4	US-09-348-578-2	Sequence 2, Appl	806	5	1.0	32	4	US-09-699-684-15	Sequence 15, Appl
734	5	1.0	27	4	US-09-345-468-21	Sequence 21, Appl	807	5	1.0	32	4	US-09-699-684-23	Sequence 23, Appl
735	5	1.0	27	4	US-08-382-452D-22	Sequence 22, Appl	808	5	1.0	32	4	US-08-737-109-22	Sequence 22, Appl
736	5	1.0	27	4	US-09-144-914-23	Sequence 23, Appl	809	5	1.0	32	4	US-09-082-358B-40	Sequence 40, Appl
737	5	1.0	27	4	US-09-227-357-291	Sequence 291, App	810	5	1.0	33	4	US-09-348-578-8	Sequence 8, Appl
738	5	1.0	27	4	US-09-414-453A-21	Sequence 21, Appl	811	5	1.0	33	4	US-09-348-578-16	Sequence 16, Appl
739	5	1.0	27	4	US-09-699-684-2	Sequence 2, Appl	812	5	1.0	33	4	US-09-348-578-24	Sequence 24, Appl
740	5	1.0	27	4	US-08-469-260A-481	Sequence 481, App	813	5	1.0	33	4	US-09-699-684-8	Sequence 8, Appl
741	5	1.0	28	1	US-08-105-483-445	Sequence 445, App	814	5	1.0	33	4	US-09-699-684-16	Sequence 16, Appl
742	5	1.0	28	1	US-08-709-209-445	Sequence 445, App	815	5	1.0	33	4	US-09-699-684-24	Sequence 24, Appl
743	5	1.0	28	1	US-08-303-275-156	Sequence 156, App	816	5	1.0	34	2	US-08-445-520B-3	Sequence 3, Appl
744	5	1.0	28	1	US-08-458-101-445	Sequence 445, App	817	5	1.0	34	3	US-08-658-136-38	Sequence 38, Appl
745	5	1.0	28	4	US-09-348-578-3	Sequence 3, Appl	818	5	1.0	34	4	US-09-348-578-9	Sequence 9, Appl
746	5	1.0	28	4	US-09-348-578-11	Sequence 11, Appl	819	5	1.0	34	4	US-09-348-578-17	Sequence 17, Appl
747	5	1.0	28	4	US-09-364-946-5	Sequence 5, Appl	820	5	1.0	34	4	US-09-348-578-25	Sequence 25, Appl
748	5	1.0	28	4	US-09-364-946-9	Sequence 9, Appl	821	5	1.0	34	4	US-09-239-864A-3	Sequence 3, Appl
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752	5	1.0	29	3	US-09-287-375-5	Sequence 5, Appl	825	5	1.0	34	4	US-09-699-684-17	Sequence 17, Appl
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831	5	1.0	35	4	US-09-315-304B-636	Sequence 636, App	904	47	3	US-09-100-600A-76	Sequence 76, Appl
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847	5	1.0	38	1	US-08-441-914-9	Sequence 9, Appl	920	48	4	US-08-817-795-65	Sequence 65, Appl
848	5	1.0	38	1	US-08-189-331-2	Sequence 2, Appl	921	48	4	US-08-448-619-8	Sequence 8, Appl
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854	5	1.0	38	2	US-08-471-800-2	Sequence 2, Appl	927	48	4	US-08-906-613-65	Sequence 65, Appl
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863	5	1.0	38	3	US-08-491-954-37	Sequence 37, Appl	936	50	3	US-09-314-093-37	Sequence 37, Appl
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999 5 1.0 2 US-08-319-866-5 Sequence 5, Appl
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ALIGNMENTS

RESULT 1
US-08-564-972-22
; Sequence 22, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Contl-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPIPTOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-22
Query Match 1.4%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
QY 132 ASRVVLS 138
Db 11 ASRVVLS 17
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; Sequence 23, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Contl-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPIPTOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
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; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
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Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
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RESULT 3
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; Sequence 74, Application US/09152060

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; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
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; EARLIER APPLICATION NUMBER: 60/040,762
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; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
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; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-74

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DB 33 RGNRRA 39

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; APPLICANT: Conti-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-564-972-8

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Query Match 1.4%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 132 ASRVVLS 138
DB 131 ASRVVLS 137

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RESULT 5
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; Sequence 27, Application US/08148058A
; Patent No. 5804407
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,058A
; FILING DATE: 04-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOL, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid

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[illegible]

NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-478-042-29

Query Match 1.4%; Score 7; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
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Db 132 ASRVLS 138

RESULT 9
US-08-645-215-27
Sequence 27, Application US/08645215
Patent No. 5827686
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,215
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,058
FILING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-645-215-27

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
|||||
Db 132 ASRVLS 138

RESULT 11
US-08-466-604-27
Sequence 27, Application US/08466604
Patent No. 5843776
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
|||||

Db 132 ASRVLS 138

RESULT 10
US-08-645-215-29
Sequence 29, Application US/08645215
Patent No. 5827686
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,215
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,058
FILING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-645-215-29

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
|||||
Db 132 ASRVLS 138

RESULT 11
US-08-466-604-27
Sequence 27, Application US/08466604
Patent No. 5843776
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
|||||
Db 132 ASRVLS 138

RESULT 11
US-08-466-604-27
Sequence 27, Application US/08466604
Patent No. 5843776
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVLS 138
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-604-27

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
Db 132 ASRVVLS 138
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RESULT 13
US-09-198-603C-8
; Sequence 8, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198.603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Human
US-09-198-603C-8

Query Match 1.4%; Score 7; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 SRLYGPS 100
Db 132 SRLYGPS 138
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RESULT 14
US-09-306-595C-8
; Sequence 8, Application US/09306595C
; Patent No. 6284506
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/306.595C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 98108210
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID-NO 8
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-306-595C-8

Query Match 1.4%; Score 7; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-604-29

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
Db 132 ASRVVLS 138
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RESULT 12
US-08-466-604-29
; Sequence 29, Application US/08466604
; Patent No. 5843776
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
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Qy 381 TTTSSSL 387
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 Db 45 TTTSSSL 51

RESULT 15

US-08-203-905B-2
 ; Sequence 2, Application US/08203905B
 ; Patent No. 5646249
 ; GENERAL INFORMATION:
 ; APPLICANT: KAYE, FEDERIC J.
 ; APPLICANT: OTTERSON, GREGORY A.
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: NOVEL CHAPERONE PROTEIN
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
 ; STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
 ; CITY: NEWPORT BEACH
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/203,905B
 ; APPLICATION NUMBER: US/08/203,905B
 ; FILING DATE: February 28, 1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KIRKPATRICK, ANITA M.
 ; REGISTRATION NUMBER: 32,617
 ; REFERENCE/DOCKET NUMBER: NIH089.001A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 471 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-203-905B-2

Query Match 1.48; Score 7; DB 1; Length 471;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DLGGGTL 72
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 Db 225 DLGGGTL 231

Search completed: April 22, 2003, 16:20:12
 Job time : 50 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:07:55 ; Search time 43 Seconds
(without alignments)
931.742 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGEWLLVLRRAARALS.....YAEVPSGHERGEFMEARQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
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- 7: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pcp.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	81.2	431	9	US-09-912-935-36
2	1295	48.1	499	9	US-09-912-935-31
3	1295	48.1	529	9	US-09-912-935-28
4	1295	48.1	529	9	US-09-912-935-40
5	1294	48.1	529	9	US-10-066-500-128
6	1294	48.1	529	9	US-10-174-590-472
7	1294	48.1	529	9	US-10-176-758-472
8	1294	48.1	529	9	US-10-175-737-472
9	1294	48.1	529	9	US-10-173-706-472
10	1294	48.1	529	9	US-10-175-738-472
11	1294	48.1	529	9	US-10-175-752-472
12	1294	48.1	529	9	US-10-176-482-472
13	1294	48.1	529	9	US-10-176-757-472
14	1294	48.1	529	9	US-10-176-913-472
15	1294	48.1	529	9	US-10-180-552-472
16	1294	48.1	529	9	US-10-180-557-472
17	1294	48.1	529	9	US-10-173-700-472
18	1294	48.1	529	9	US-10-174-572-472
19	1294	48.1	529	9	US-10-174-579-472

ALIGNMENTS

RESULT 1

US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match 81.2%; Score 2185; DB 9; Length 431;

Best Local Similarity 95.2%; Pred. No. 8.7e-189;

Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	72	LAMDPLPNRTFVVDNHSYVSRLYGPSEPHSRELWVDVAEANKRSQVKIHTILSNTHRQ	131
Db	1	LAMDPLPNRTFVVDNHSYVSRLYGPSEPHSRELWVDVAEANKRSQVKIHTILSNTHRQ	60
Qy	132	ASRVLSFDFPFYGHPLRQITATGTFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	191
Db	61	ASRVLSFDFPFYGHPLRQITATGTFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	120
Qy	192	VYFONGTVFVQVWDHVYVQWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSSQHP	251
Db	121	VYFONGTVFVQVWDHVYVQWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSSQHP	180
Qy	252	VKTGLSDFAMILNPSDPVPESSRRSIFFYHRIELDPKSVTSMSAVEFTPLTCLQHRSCD	311
Db	181	VKTGLSDFAMILNPSDPVPESSRRSIFFYHRIELDPKSVTSMSAVEFTPLTCLQHRSCD	240
Qy	312	ACMSSDLTFNCWCHVLQRCSSGDFRYRQEW-MDYGCAQAEGRMCEDFQD-----ED	363

Db 241 ACMSSDLTFCNSWCHVLRQCSGSDRYRQWGDGTGCAQAEAG-----QDVRLPGMRT 294
QY 364 HDSASPDTSFSPYDGLTSSFLIDSLTDDTKLNPYAGDGLONNLSPKTKGTPVH 423
Db 295 TTSASPDTSFSPYDGLTSSFLIDSLTDDTKLNPYAGDGLONNLSPKTKGTPVH 354
QY 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAE 483
Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAE 414
QY 484 VEPSGHEKEGMEABQC 500
Db 415 VEPSGHEKEGMEABQC 431

RESULT 2

US-09-912-935-31
; Sequence 31, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-31

Query Match 48.1%; Score 1295; DB 9; Length 499;
Best Local Similarity 57.3%; Pred. No. 2.1e-108;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSEPHSRELWVDVAEANRSOVKIHILSNTHR 130
Db 65 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDLWNIDQMEKDKVKIHILSNTHR 124
QY 131 QASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSDNS 190
Db 125 QAARVNLSDFAFVVVHRIQIIPNVRRTIYEHVRLVMTATQYIAPLMANFNPYSDNS 184
QY 191 TVVYFDNGTVFVQWHDVYVLRQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 185 TVRYFDNGTALVQWHDVHVLQDNYNLGSTFTQATLLMDGRIIFGYKEIPVLVTOISSTNH 244
QY 251 PVKGLSDAFMILNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 310
Db 245 PVKGLSDAFVVRHRIQIIPNVRRTIYEHVRLVMTATQYIAPLMANFNPYSDNS 304
QY 311 DACMSSDLTFCNSWCHVLRQCSGSDRYRQWGDGTGCAQAEAGRMCEDFODEDHSDASPD 370
Db 305 GPCVSSQIGFNCWSKLRQCSGSDRYRQWGDGTGCAQAEAGRMCEDFODEDHSDASPD 364
QY 371 T--SFSPYDGLTSS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 365 TIGATTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKDNASTDSSAEKKGTLHA 424
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 425 GLVIGLILVILVATAILVTVMYHHPTSAASIFPIERRPSRWPMKFRSGHGPAYAEV 484
QY 485 EPSGHEKEGMEABQC 500
Db 485 EPVG-EKEGFIVSEQ 499

RESULT 3

US-09-912-935-28
; Sequence 28, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-28

Query Match 48.1%; Score 1295; DB 9; Length 529;
Best Local Similarity 57.3%; Pred. No. 2.3e-108;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSEPHSRELWVDVAEANRSOVKIHILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDLWNIDQMEKDKVKIHILSNTHR 154
QY 131 QASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSDNS 190
Db 155 QAARVNLSDFAFVVVHRIQIIPNVRRTIYEHVRLVMTATQYIAPLMANFNPYSDNS 214
QY 191 TVVYFDNGTVFVQWHDVYVLRQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVQWHDVHVLQDNYNLGSTFTQATLLMDGRIIFGYKEIPVLVTOISSTNH 274
QY 251 PVKGLSDAFMILNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 310
Db 275 PVKGLSDAFVVRHRIQIIPNVRRTIYEHVRLVMTATQYIAPLMANFNPYSDNS 334
QY 311 DACMSSDLTFCNSWCHVLRQCSGSDRYRQWGDGTGCAQAEAGRMCEDFODEDHSDASPD 370
Db 335 GPCVSSQIGFNCWSKLRQCSGSDRYRQWGDGTGCAQAEAGRMCEDFODEDHSDASPD 394
QY 371 T--SFSPYDGLTSS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TIGATTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKDNASTDSSAEKKGTLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 455 GLVIGLILVILVATAILVTVMYHHPTSAASIFPIERRPSRWPMKFRSGHGPAYAEV 514
QY 485 EPSGHEKEGMEABQC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 4

US-09-912-935-40
; Sequence 40, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53

[illegible]

150	QY	QASRVLSFDFPFYGHPLROITATGCFIFMGDVIHRLTATQYAPLMAFNPGVSDNS	190
151	QY		191
152	QY		192
153	QY		193
154	QY		194
155	QY	QARVLSFDFPFYGHFLREITVATGCFYGEVWHRLTATQYIAPLMAFNDFPSVRNS	214
156	QY		215
157	QY		216
158	QY		217
159	QY	TVVYFDNGTVFYVQWDHVLQGHEDKGSFTFQALHHGGRIVFYAKELPMSVPEISSOH	250
160	QY		251
161	QY		252
162	QY		253
163	QY	TVRFDSGTALVQWDHVLQGDNYNLGSFTTFQATLLMGRIHIFGYKELPVLVQVISTNH	274
164	QY		275
165	QY		276
166	QY		277
167	QY		278
168	QY		279
169	QY		280
170	QY		281
171	QY		282
172	QY		283
173	QY		284
174	QY		285
175	QY		286
176	QY		287
177	QY		288
178	QY		289
179	QY		290
180	QY		291
181	QY		292
182	QY		293
183	QY		294
184	QY		295
185	QY		296
186	QY		297
187	QY		298
188	QY		299
189	QY		300

[illegible]

```

, APPLICANT: Desnoyers, Luc
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Gurney, Austin L.
, APPLICANT: Pan, James
, APPLICANT: Smith, Victoria
, APPLICANT: Watanabe, Colin K.
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID SEQUENCES
, FILE REFERENCE: P3430R1C50
, CURRENT APPLICATION NUMBER: US/110/175,737
, CURRENT FILING DATE: 2002-06-19
, Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-175-737-472

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Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels

[illegible]

RESULT 9

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US-10-173-706-472
; Sequence 472, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSFERRED
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-472

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ORGANISM: HOMINID
US-10-173-706-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels

Qy	72	LAMDTLPDNRTRVVED-NHSYVYGRLYGSPSPHRELVWDVAEANKRSQVKIHTILSNTHR	130
Db	95	LLLDQGDQNNFQIEDTDHNYIISRIYCPDSASDRDLWNIDQMEKDKVKIHGILSNTHR	154
Qy	131	QASRVLSFDFPFVGHPLRQIITATGCFIEMGDVTHRLMTATQYVAPLMAFNPNPGYSDNS	190
Db	155	QAARVNSLDFPFVGHREILVTATGGFITGEVWHRLMTATQIAPLMAFNFPSPVSRNS	214
Qy	191	TVVYFDNGTVFVQWDMHYVLQGWEDKGSFTQAAHLHDGRIVFAFYKEIPMSVPEIISSSOH	250
Db	215	TVRYFDNGTALVQWDMHVHLQDYNLNGSFTFOATLLMDGRIIFGYKEIPVLVQIISSTNH	274
Qy	251	PVKYGLSDAFMLNPSDPVPSRRRSITFEYHRELDPSKVTSMASVEFPTLPCLQHRSC	310
Db	275	PVKYGLSDAFVWHRIQOIPNRRRTIYEYHRELOQSKITNISAVEMTLPCLQFNRC	334
Qy	311	DACMSSDLTNCMCHVQLQCSCGFDRYRQEWMDYGCQAQEAEGRMCEDFODEDHDSASP	370
Db	335	GPCVSSQIGFNCMCSKLCRCSCGFDRHRQDWNVDSGCPPEESKEKMCENTEPVTSRTTIT	394
Qy	371	T--SFSYDGDLLTTS---SSLFIDSJLTTEDDTKLNPYAGGDGLQ--NNLSPKTGTPVHL	424
Db	395	TVGATTTQFRLTTTRRAVTSQFPTSLPTSEDDTKIALHLKDNCGASTDSDAAEEKGGTLHA	454
Qy	425	GTIVGIVLAVLVAAILAGIYNGHTPSNAALFFTERRRPHHPAMKFRSHDPHSTYAEV	484
Db	455	GLIIGILLLVIVATALLVTVYWHHTPSAASIFFTERRPSRPAMKFRSGCHPAIEV	514
Qy	485	EPSGHEKEGFMBAQC	500
Db	515	EPVG-EKEGFIVSEQ	529

RESULT 10

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US-10-175-738-472
; Sequence 472, Application US/10175738
; Publication No. US20030022294A1
;
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRAN
; TITLE OF INVENTION: ACIDS ENCODING ?
; FILE REFERENCE: P3430RIC45
; CURRENT APPLICATION NUMBER: US/10/17
; CURRENT FILING DATE: 2002-06-19
; prior application removed - See File
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-472

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Query Match	48.1%;	Score 1294;	DB 9;	Length 529;
Best Local Similarity	57.1%;	Pred. No. 2.9e-108;		

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Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSCGPEESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKONGASTDDSAAEKKGTLHA 454
Qy 425 GTIVGIVLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPWPAKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMEEAEOC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 13

US-10-176-757-472

; Sequence 472, Application US/10176757

; Publication No. US20030022297A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C86

; CURRENT APPLICATION NUMBER: US/10/176,757

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-757-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSEPHSRELWVDAEANKRSQVKIHTILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTHNYIISRIYGPDSASRDWVNDQMEKDKVKIHLGILSNTHR 154
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMANFNPYSDNS 190
Db 155 QAARVNLSDFFPFYGHPLREITATGGFIYGVVHRMLTATQYIAPLMANFNPYSDNS 214
Qy 191 TVVYFDNGTFFVVDWVHVHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVVDWVHVHVLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVQISSTNH 274
Qy 251 PVKTLGLDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLOHRS 310
Db 275 PVKGLSDAFVWVHRIQIIPNVRRRIIYEHVRELQMSKITNISAVEMTPLPTCLOFNRC 334
Qy 311 DACMSSDLTFCNCHWCHVLRQCSGDFRYRQEWMDYCAOAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSCGPEESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKONGASTDDSAAEKKGTLHA 454

Qy 425 GTIVGIVLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPWPAKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMEEAEOC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 14

US-10-176-913-472

; Sequence 472, Application US/10176913

; Publication No. US20030022298A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C66

; CURRENT APPLICATION NUMBER: US/10/176,913

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-913-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSEPHSRELWVDAEANKRSQVKIHTILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTHNYIISRIYGPDSASRDWVNDQMEKDKVKIHLGILSNTHR 154
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMANFNPYSDNS 190
Db 155 QAARVNLSDFFPFYGHPLREITATGGFIYGVVHRMLTATQYIAPLMANFNPYSDNS 214
Qy 191 TVVYFDNGTFFVVDWVHVHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVVDWVHVHVLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVQISSTNH 274
Qy 251 PVKTLGLDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLOHRS 310
Db 275 PVKGLSDAFVWVHRIQIIPNVRRRIIYEHVRELQMSKITNISAVEMTPLPTCLOFNRC 334
Qy 311 DACMSSDLTFCNCHWCHVLRQCSGDFRYRQEWMDYCAOAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSCGPEESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKONGASTDDSAAEKKGTLHA 454
Qy 425 GTIVGIVLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPWPAKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMEEAEOC 500
Db 515 EPVG-EKEGFIVSEQ 529

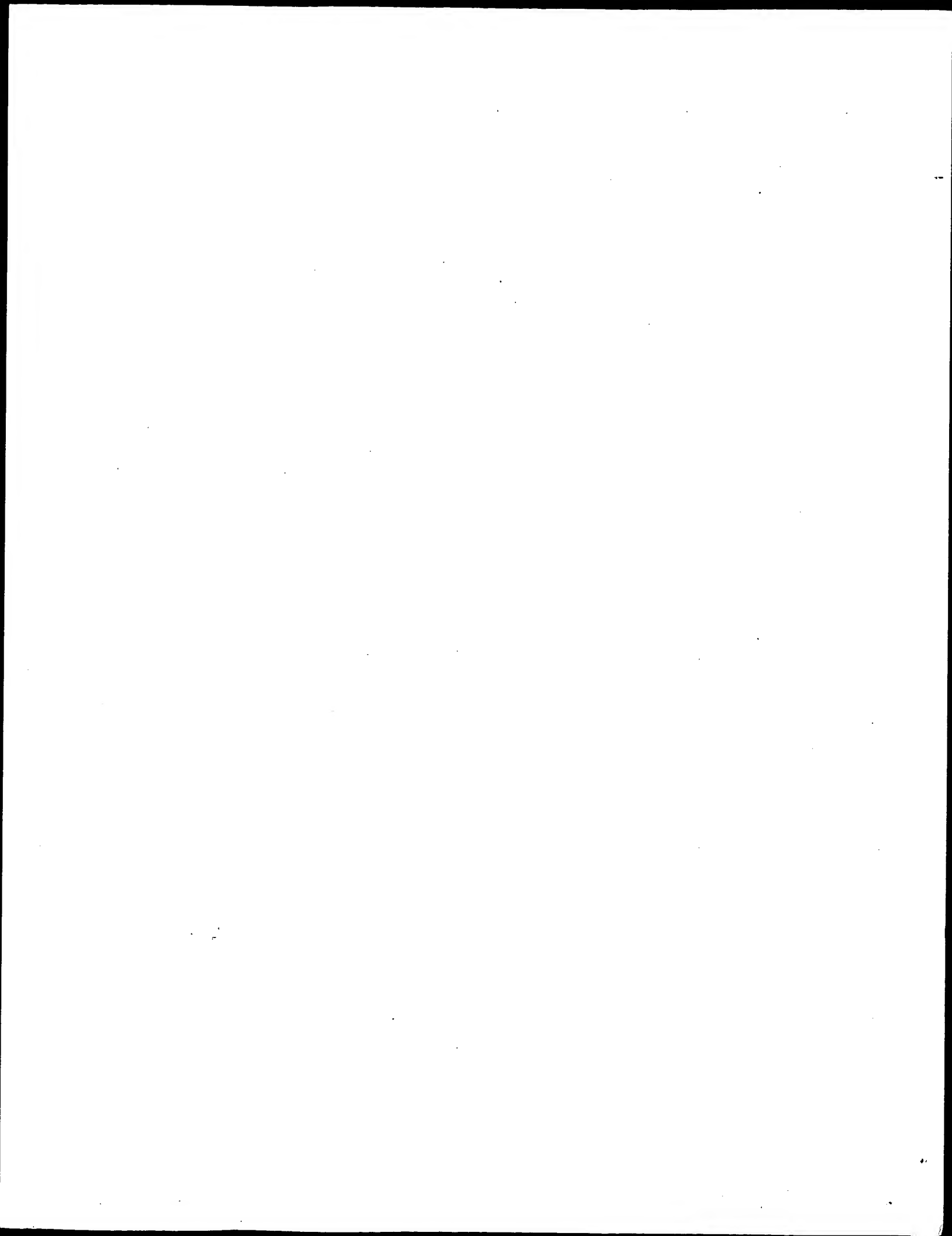
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; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC153
; CURRENT APPLICATION NUMBER: US/10/180,552
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-180-552-472

Query Match      48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVED-NHSYVYVSRLYGSPSEPHRELWVDVAEANRSQVKIHTILSNTHR 130
DB 95 LLLDDGDQNDNTQIEDTHNYIYISRIYGPSDSASRDVAWNIDOMEKDKVKINGILSNTHR 154
QY 131 QASRVVLSDFPFYGHPLRQIATGTFMGDVTHRLMTATQYVAPLMANENPGYSNDS 190
DB 155 QAARVNLSPDFPFYGHFLREITVATGGFTYTGTVHRLMTATQYIAPLMANFDPVSVRNS 214
QY 191 TVYFDNGTVFVQVDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
DB 215 TVRYFDNGTALVQVDHVLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVQLSSNTH 274
QY 251 PVKTGLSDAFMILNPSDPVPSERRRSIFEYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 310
DB 275 PVKVGSLDAFVVVHRIQIPNVRRRTIYEHVRELQMSKITNISAVEMTPTCLQFNRC 334
QY 311 DACMSSDLFNCWCHVLQRCSSGDRYQENWMDYCAQEAERWCEDFQDEDDHDSASPD 370
DB 335 GPCVSSQIGFNCWCSKQRCSSGDRYQENWMDYCAQEAERWCEDFQDEDDHDSASPD 394
QY 371 T--SFSFYDGLTFTS---SSLFIDSLTDEDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
DB 395 TVGATTQFVLTTRAVTSQPTSLPTEDDTKIALHLKDNKNGASTDDSAEKKGGTLHA 454
QY 425 GTTIVGIVLAVLLAGIYINGHTPSNAALFFIERRPHIHWPAKFKRSHDPDHSYAEV 484
DB 455 GLIIGILILVIVATILVTVMYHHPTSAASIFFIERRPSRWPAMKFRRGSGHPAYAEV 514
QY 485 EPSGHEKEGMEAEQC 500
DB 515 EPVG-EKEGFIVSEQC 529
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Search completed: April 22, 2003, 16:15:41
Job time : 45 secs



GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 16:18:56 ; Search time 20 Seconds

(without alignments)
2003.245 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

Sequence: 1 MKGELWLLVLRLREARALS.....YAEVEPSGHEKEGFMEARQC 500

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 301932 seqs, 80129803 residues

Word size : 0

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:

1: /cgn2_5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271	54.2	431	9	US-09-912-935-36
2	53	10.6	53	10	US-09-864-761-43750
3	10	2.0	118	10	US-09-867-550-198
4	10	2.0	392	9	US-09-912-935-23
5	10	2.0	392	9	US-09-912-935-25
6	10	2.0	425	9	US-09-912-935-35
7	10	2.0	449	9	US-09-912-935-34
8	10	2.0	499	9	US-09-912-935-31
9	10	2.0	529	9	US-10-066-500-128
10	10	2.0	529	9	US-10-174-590-472
11	10	2.0	529	9	US-10-176-758-472
12	10	2.0	529	9	US-10-175-737-472
13	10	2.0	529	9	US-09-912-935-28
14	10	2.0	529	9	US-09-912-935-40
15	10	2.0	529	9	US-10-173-706-472
16	10	2.0	529	9	US-10-175-738-472
17	10	2.0	529	9	US-10-175-752-472
18	10	2.0	529	9	US-10-176-482-472
19	10	2.0	529	9	US-10-176-757-472
20	10	2.0	529	9	US-10-176-913-472
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28	10	2.0	529	9	US-10-175-739-472
29	10	2.0	529	9	US-10-175-743-472
30	10	2.0	529	9	US-10-176-488-472
31	10	2.0	529	9	US-10-176-492-472
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67	10	2.0	529	9	US-10-184-646-472
68	10	2.0	529	9	US-10-184-647-472
69	10	2.0	529	9	US-10-184-652-472
70	10	2.0	529	9	US-10-184-654-472
71	10	2.0	529	9	US-10-187-594-472
72	10	2.0	529	9	US-10-187-596-472
73	10	2.0	529	9	US-10-187-745-472
74	10	2.0	529	9	US-10-187-885-472
75	10	2.0	529	9	US-10-187-886-472
76	10	2.0	529	9	US-10-187-887-472
77	10	2.0	529	9	US-10-187-888-472
78	10	2.0	529	9	US-10-187-889-472
79	10	2.0	529	9	US-10-187-890-472
80	10	2.0	529	9	US-10-187-891-472
81	10	2.0	529	9	US-10-187-892-472
82	10	2.0	529	9	US-10-187-893-472
83	10	2.0	529	9	US-10-187-894-472
84	10	2.0	529	9	US-10-187-895-472
85	10	2.0	529	9	US-10-187-896-472
86	10	2.0	529	9	US-10-187-897-472
87	10	2.0	529	9	US-10-187-898-472
88	10	2.0	529	9	US-10-187-899-472
89	10	2.0	529	9	US-10-187-900-472
90	10	2.0	529	9	US-10-187-901-472
91	10	2.0	529	9	US-10-187-902-472
92	10	2.0	529	9	US-10-187-903-472
93	10	2.0	529	9	US-10-187-904-472
94	10	2.0	529	9	US-10-187-905-472
95	10	2.0	529	9	US-10-187-906-472
96	10	2.0	529	9	US-10-187-907-472
97	10	2.0	529	9	US-10-187-908-472
98	10	2.0	529	9	US-10-187-909-472
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93	10	2.0	529	9	US-10-183-013-472	Sequence 472, App	166	10	2.0	529	9	US-10-176-484-472	Sequence 472, App
94	10	2.0	529	9	US-10-184-612-472	Sequence 472, App	167	10	2.0	529	9	US-10-176-753-472	Sequence 472, App
95	10	2.0	529	9	US-10-184-616-472	Sequence 472, App	168	10	2.0	529	9	US-10-176-917-472	Sequence 472, App
96	10	2.0	529	9	US-10-184-617-472	Sequence 472, App	169	10	2.0	529	9	US-10-176-982-472	Sequence 472, App
97	10	2.0	529	9	US-10-184-622-472	Sequence 472, App	170	10	2.0	529	9	US-10-179-506-472	Sequence 472, App
98	10	2.0	529	9	US-10-184-628-472	Sequence 472, App	171	10	2.0	529	9	US-10-179-513-472	Sequence 472, App
99	10	2.0	529	9	US-10-184-629-472	Sequence 472, App	172	10	2.0	529	9	US-10-179-514-472	Sequence 472, App
100	10	2.0	529	9	US-10-184-630-472	Sequence 472, App	173	10	2.0	529	9	US-10-179-522-472	Sequence 472, App
101	10	2.0	529	9	US-10-184-631-472	Sequence 472, App	174	10	2.0	529	9	US-10-180-556-472	Sequence 472, App
102	10	2.0	529	9	US-10-184-632-472	Sequence 472, App	175	10	2.0	529	9	US-10-180-560-472	Sequence 472, App
103	10	2.0	529	9	US-10-184-636-472	Sequence 472, App	176	10	2.0	529	9	US-10-183-015-472	Sequence 472, App
104	10	2.0	529	9	US-10-184-640-472	Sequence 472, App	177	10	2.0	529	9	US-10-184-615-472	Sequence 472, App
105	10	2.0	529	9	US-10-184-650-472	Sequence 472, App	178	10	2.0	529	9	US-10-184-620-472	Sequence 472, App
106	10	2.0	529	9	US-10-184-651-472	Sequence 472, App	179	10	2.0	529	9	US-10-184-643-472	Sequence 472, App
107	10	2.0	529	9	US-10-187-588-472	Sequence 472, App	180	10	2.0	529	9	US-10-184-656-472	Sequence 472, App
108	10	2.0	529	9	US-10-187-597-472	Sequence 472, App	181	10	2.0	529	9	US-10-192-010-472	Sequence 472, App
109	10	2.0	529	9	US-10-187-598-472	Sequence 472, App	182	10	2.0	529	9	US-10-195-894-472	Sequence 472, App
110	10	2.0	529	9	US-10-187-600-472	Sequence 472, App	183	10	2.0	529	9	US-10-205-908-472	Sequence 472, App
111	10	2.0	529	9	US-10-187-603-472	Sequence 472, App	184	10	2.0	529	9	US-10-184-619-472	Sequence 472, App
112	10	2.0	529	9	US-10-187-603-472	Sequence 472, App	185	10	2.0	529	9	US-10-186-855-472	Sequence 472, App
113	10	2.0	529	9	US-10-187-741-472	Sequence 472, App	186	10	2.0	529	9	US-10-187-599-472	Sequence 472, App
114	10	2.0	529	9	US-10-187-743-472	Sequence 472, App	187	10	2.0	529	9	US-10-187-750-472	Sequence 472, App
115	10	2.0	529	9	US-10-187-743-472	Sequence 472, App	188	10	2.0	529	9	US-10-188-780-472	Sequence 472, App
116	10	2.0	529	9	US-10-187-746-472	Sequence 472, App	189	10	2.0	529	9	US-10-192-015-472	Sequence 472, App
117	10	2.0	529	9	US-10-187-747-472	Sequence 472, App	190	10	2.0	529	9	US-10-194-394-472	Sequence 472, App
118	10	2.0	529	9	US-10-187-751-472	Sequence 472, App	191	10	2.0	529	9	US-10-194-425-472	Sequence 472, App
119	10	2.0	529	9	US-10-187-753-472	Sequence 472, App	192	10	2.0	529	9	US-10-194-485-472	Sequence 472, App
120	10	2.0	529	9	US-10-187-754-472	Sequence 472, App	193	10	2.0	529	9	US-10-195-885-472	Sequence 472, App
121	10	2.0	529	9	US-10-187-757-472	Sequence 472, App							

385	10	2.0	529	9	US-10-207-924-472	Sequence 472, App	458	7	1.4	1184	9	US-09-990-726-124	Sequence 124, App
386	10	2.0	529	9	US-10-208-028-472	Sequence 472, App	459	7	1.4	1184	9	US-09-997-559-124	Sequence 124, App
387	10	2.0	529	12	US-10-052-586-472	Sequence 472, App	460	7	1.4	1184	9	US-09-997-601-124	Sequence 124, App
388	10	2.0	530	9	US-09-912-935-38	Sequence 38, Appl	461	7	1.4	1184	9	US-10-121-050-412	Sequence 412, App
389	7	1.4	72	9	US-10-178-213-425	Sequence 425, App	462	7	1.4	1184	9	US-10-141-755-412	Sequence 412, App
390	7	1.4	74	10	US-09-852-797-74	Sequence 74, Appl	463	7	1.4	1184	9	US-09-989-729A-124	Sequence 124, App
391	7	1.4	74	10	US-09-852-797-74	Sequence 74, Appl	464	7	1.4	1184	9	US-09-990-440-124	Sequence 124, App
392	7	1.4	74	10	US-09-852-797-74	Sequence 74, Appl	465	7	1.4	1184	9	US-09-991-854-124	Sequence 124, App
393	7	1.4	74	10	US-09-852-797-74	Sequence 74, Appl	466	7	1.4	1184	9	US-09-997-349-124	Sequence 124, App
394	7	1.4	77	10	US-09-864-761-46115	Sequence 74, Appl	467	7	1.4	1184	9	US-09-997-440-124	Sequence 124, App
395	7	1.4	78	10	US-09-867-550-1402	Sequence 1402, App	468	7	1.4	1184	9	US-09-997-628-124	Sequence 124, App
396	7	1.4	99	10	US-09-915-582-54	Sequence 54, Appl	469	7	1.4	1184	9	US-09-997-683-124	Sequence 124, App
397	7	1.4	110	10	US-09-740-668A-14	Sequence 14, Appl	470	7	1.4	1184	9	US-10-143-032-412	Sequence 412, App
398	7	1.4	110	10	US-09-915-582-70	Sequence 70, Appl	471	7	1.4	1184	9	US-09-993-469-124	Sequence 124, App
399	7	1.4	270	9	US-09-738-626-5868	Sequence 5868, App	472	7	1.4	1184	9	US-09-993-742-124	Sequence 124, App
400	7	1.4	299	9	US-10-123-540-388	Sequence 388, App	473	7	1.4	1184	9	US-09-997-548-124	Sequence 124, App
401	7	1.4	299	10	US-09-764-870-388	Sequence 388, App	474	7	1.4	1184	9	US-10-123-108-412	Sequence 412, App
402	7	1.4	313	9	US-10-102-806-741	Sequence 741, App	475	7	1.4	1184	9	US-10-123-236-412	Sequence 412, App
403	7	1.4	330	9	US-09-984-245-203	Sequence 203, App	476	7	1.4	1184	9	US-10-123-261-412	Sequence 412, App
404	7	1.4	330	9	US-09-966-262-203	Sequence 203, App	477	7	1.4	1184	9	US-10-123-261-412	Sequence 412, App
405	7	1.4	330	9	US-09-983-966-203	Sequence 203, App	478	7	1.4	1184	9	US-10-140-921-412	Sequence 412, App
406	7	1.4	330	9	US-10-143-090-203	Sequence 203, App	479	7	1.4	1184	9	US-10-140-928-412	Sequence 412, App
407	7	1.4	388	10	US-09-815-242-11458	Sequence 11458, A	480	7	1.4	1184	9	US-09-990-427-124	Sequence 124, App
408	7	1.4	388	10	US-09-815-242-11623	Sequence 11623, A	481	7	1.4	1184	9	US-10-121-045-412	Sequence 412, App
409	7	1.4	417	9	US-09-935-642-7	Sequence 7, Appl	482	7	1.4	1184	9	US-10-123-292-412	Sequence 412, App
410	7	1.4	419	10	US-09-925-300-1506	Sequence 1506, App	483	7	1.4	1184	9	US-10-123-903-412	Sequence 412, App
411	7	1.4	423	9	US-09-738-626-3570	Sequence 3570, App	484	7	1.4	1184	9	US-10-124-819-412	Sequence 412, App
412	7	1.4	432	9	US-09-925-388-8	Sequence 8, Appl	485	7	1.4	1184	9	US-10-124-822-412	Sequence 412, App
413	7	1.4	498	9	US-09-557-796-26	Sequence 26, Appl	486	7	1.4	1184	9	US-10-140-925-412	Sequence 412, App
414	7	1.4	520	9	US-10-157-855-2	Sequence 2, Appl	487	7	1.4	1184	9	US-10-160-498-412	Sequence 412, App
415	7	1.4	520	9	US-10-223-076-3	Sequence 3, Appl	488	7	1.4	1184	10	US-09-757-716-3	Sequence 3, Appl
416	7	1.4	535	9	US-10-224-209-2	Sequence 2, Appl	489	7	1.4	1184	10	US-09-989-722-124	Sequence 124, App
417	7	1.4	742	9	US-09-104-408-33	Sequence 33, Appl	490	7	1.4	1184	10	US-09-989-723-124	Sequence 124, App
418	7	1.4	924	9	US-10-108-605-137	Sequence 137, App	491	7	1.4	1184	10	US-09-989-729-124	Sequence 124, App
419	7	1.4	1184	9	US-09-989-293A-124	Sequence 124, App	492	7	1.4	1184	10	US-09-989-727-124	Sequence 124, App
420	7	1.4	1184	9	US-09-989-735-124	Sequence 124, App	493	7	1.4	1184	10	US-09-989-731-124	Sequence 124, App
421	7	1.4	1184	9	US-09-989-735-124	Sequence 124, App	494	7	1.4	1184	10	US-09-989-732-124	Sequence 124, App
422	7	1.4	1184	9	US-09-989-735-124	Sequence 124, App	495	7	1.4	1184	10	US-09-991-073-124	Sequence 124, App
423	7	1.4	1184	9	US-09-989-730-124	Sequence 124, App	496	7	1.4	1184	10	US-09-990-442-124	Sequence 124, App
424	7	1.4	1184	9	US-09-989-730-124	Sequence 124, App	497	7	1.4	1184	10	US-09-991-163-124	Sequence 124, App
425	7	1.4	1184	9	US-09-990-436-124	Sequence 124, App	498	7	1.4	1184	10	US-09-991-604-124	Sequence 124, App
426	7	1.4	1184	9	US-09-991-181-124	Sequence 124, App	499	7	1.4	1184	10	US-09-990-456-124	Sequence 124, App
427	7	1.4	1184	9	US-09-993-687-124	Sequence 124, App	500	7	1.4	1184	10	US-09-989-721-124	Sequence 124, App
428	7	1.4	1184	9	US-09-989-734-124	Sequence 124, App	501	7	1.4	1223	9	US-10-059-962-2	Sequence 2, Appl
429	7	1.4	1184	9	US-10-028-072-412	Sequence 412, App	502	7	1.4	1421	9	US-10-014-717-2	Sequence 2, Appl
430	7	1.4	1184	9	US-09-993-667-124	Sequence 124, App	503	6	1.2	17	10	US-09-945-258-19	Sequence 19, Appl
431	7	1.4	1184	9	US-10-121-049-412	Sequence 412, App	504	6	1.2	28	10	US-09-864-761-47084	Sequence 47084, A
432	7	1.4	1184	9	US-10-123-904-412	Sequence 412, App	505	6	1.2	30	9	US-10-010-114-18	Sequence 18, Appl
433	7	1.4	1184	9	US-10-140-470-412	Sequence 412, App	506	6	1.2	33	10	US-09-975-901-17	Sequence 17, Appl
434	7	1.4	1184	9	US-09-990-438-124	Sequence 124, App	507	6	1.2	34	10	US-09-864-761-40527	Sequence 40527, A
435	7	1.4	1184	9	US-09-990-562-124	Sequence 124, App	508	6	1.2	43	9	US-10-016-157A-160	Sequence 160, App
436	7	1.4	1184	9	US-09-997-428-124	Sequence 124, App	509	6	1.2	44	10	US-09-864-761-33650	Sequence 33650, A
437	7	1.4	1184	9	US-09-997-666-124	Sequence 124, App	510	6	1.2	44	10	US-09-864-761-42079	Sequence 42079, A
438	7	1.4	1184	9	US-10-175-746-412	Sequence 412, App	511	6	1.2	44	10	US-09-815-242-12465	Sequence 12465, A
439	7	1.4	1184	9	US-10-176-918-412	Sequence 412, App	512	6	1.2	44	10	US-09-815-242-13019	Sequence 13019, A
440	7	1.4	1184	9	US-10-176-918-412	Sequence 412, App	513	6	1.2	45	9	US-09-798-889-72	Sequence 72, Appl
441	7	1.4	1184	9	US-09-990-711-124	Sequence 124, App	514	6	1.2	54	10	US-09-864-761-42619	Sequence 42619, A
442	7	1.4	1184	9	US-10-137-865-412	Sequence 412, App	515	6	1.2	54	10	US-09-764-877-1220	Sequence 1220, App
443	7	1.4	1184	9	US-10-140-474-412	Sequence 412, App	516	6	1.2	56	10	US-09-815-242-5765	Sequence 5765, App
444	7	1.4	1184	9	US-10-142-431-412	Sequence 412, App	517	6	1.2	58	9	US-10-078-107-8	Sequence 8, Appl
445	7	1.4	1184	9	US-10-143-114-412	Sequence 114, App	518	6	1.2	58	9	US-10-077-751-8	Sequence 8, Appl
446	7	1.4	1184	9	US-09-989-726-124	Sequence 124, App	519	6	1.2	59	10	US-09-864-761-40502	Sequence 40502, A
447	7	1.4	1184	9	US-10-140-002-412	Sequence 412, App	520	6	1.2	60	10	US-09-864-761-34827	Sequence 34827, A
448	7	1.4	1184	9	US-09-990-437-124	Sequence 124, App	521	6	1.2	62	10	US-09-864-761-35624	Sequence 35624, A
449	7	1.4	1184	9	US-09-998-156-124	Sequence 124, App	522	6	1.2	64	9	US-10-145-415-36	Sequence 36, Appl
450	7	1.4	1184	9	US-10-142-419-412	Sequence 412, App	523	6	1.2	64	9	US-10-145-415-38	Sequence 38, Appl
451	7	1.4	1184	9	US-09-991-157-124	Sequence 124, App	524	6	1.2	65	9	US-09-738-626-4248	Sequence 4248, App
452	7	1.4	1184	9	US-09-991-172-124	Sequence 124, App	525	6	1.2	72	10	US-09-864-761-40816	Sequence 40816, A
453	7	1.4	1184	9	US-09-997-514-124	Sequence 124, App	526	6	1.2	73	9	US-09-738-626-6672	Sequence 6672, App
454	7	1.4	1184	9	US-09-997-573-124	Sequence 124, App	527	6	1.2	74	9	US-09-813-153-111	Sequence 111, App
455	7	1.4	1184	9	US-10-123-262-412	Sequence 412, App	528	6	1.2	76	9	US-09-776-724A-135	Sequence 135, App
456	7	1.4	1184	9	US-10-142-423-412	Sequence 412, App	529	6	1.2	83	10	US-09-764-864-907	Sequence 907, App
457	7	1.4	1184	9	US-09-990-443-124	Sequence 124, App	530	6	1.2	88	10	US-09-864-761-46888	Sequence 46888, A

531	6	1.2	89	10	US-09-915-582-76	Sequence 76, Appl	604	1.2	226	9	US-09-992-598-151	Sequence 151, App
532	6	1.2	90	9	US-10-083-357-1282	Sequence 1282, Ap	605	1.2	226	9	US-09-989-233A-151	Sequence 151, App
533	6	1.2	91	9	US-09-738-626-6912	Sequence 6912, Ap	606	1.2	226	9	US-09-989-735-151	Sequence 151, App
534	6	1.2	92	10	US-09-939-980-340	Sequence 340, App	607	1.2	226	9	US-09-990-444-151	Sequence 151, App
535	6	1.2	93	10	US-09-764-864-1203	Sequence 1203, Ap	608	1.2	226	9	US-09-989-730-151	Sequence 151, App
536	6	1.2	98	12	US-10-001-879-146	Sequence 146, App	609	1.2	226	9	US-09-990-436-151	Sequence 151, App
537	6	1.2	99	10	US-09-864-761-42807	Sequence 42807, A	610	1.2	226	9	US-09-991-181-151	Sequence 151, App
538	6	1.2	100	9	US-10-045-180A-11	Sequence 11, Appl	611	1.2	226	9	US-09-993-687-151	Sequence 151, App
539	6	1.2	104	10	US-09-864-761-45427	Sequence 45427, A	612	1.2	226	9	US-09-989-734-151	Sequence 151, App
540	6	1.2	105	9	US-10-091-504-1175	Sequence 1175, Ap	613	1.2	226	9	US-09-997-653-151	Sequence 151, App
541	6	1.2	105	10	US-09-764-869-1175	Sequence 1175, Ap	614	1.2	226	9	US-10-174-590-122	Sequence 122, App
542	6	1.2	107	10	US-09-867-550-282	Sequence 282, App	615	1.2	226	9	US-10-176-758-122	Sequence 122, App
543	6	1.2	109	9	US-09-796-692-2460	Sequence 2460, Ap	616	1.2	226	9	US-10-175-737-122	Sequence 122, App
544	6	1.2	109	10	US-09-864-761-33601	Sequence 33601, A	617	1.2	226	9	US-09-993-667-151	Sequence 151, App
545	6	1.2	112	9	US-10-101-464A-535	Sequence 535, App	618	1.2	226	9	US-10-173-706-122	Sequence 122, App
546	6	1.2	117	9	US-09-949-842-17	Sequence 17, Appl	619	1.2	226	9	US-10-175-732-122	Sequence 122, App
547	6	1.2	121	9	US-09-738-626-4106	Sequence 4106, Ap	620	1.2	226	9	US-10-176-482-122	Sequence 122, App
548	6	1.2	121	9	US-09-820-843A-118	Sequence 118, App	621	1.2	226	9	US-10-176-757-122	Sequence 122, App
549	6	1.2	121	10	US-09-925-297-791	Sequence 791, App	622	1.2	226	9	US-10-176-913-122	Sequence 122, App
550	6	1.2	122	9	US-10-125-540-321	Sequence 321, App	623	1.2	226	9	US-10-175-738-122	Sequence 122, App
551	6	1.2	122	10	US-09-764-870-321	Sequence 321, App	624	1.2	226	9	US-10-175-732-122	Sequence 122, App
552	6	1.2	122	10	US-09-764-853-636	Sequence 636, App	625	1.2	226	9	US-10-176-482-122	Sequence 122, App
553	6	1.2	122	10	US-09-925-300-1438	Sequence 1438, Ap	626	1.2	226	9	US-10-176-913-122	Sequence 122, App
554	6	1.2	125	9	US-09-918-508-7	Sequence 7, Appl	627	1.2	226	9	US-10-176-757-122	Sequence 122, App
555	6	1.2	132	9	US-09-975-036-9	Sequence 9, Appl	628	1.2	226	9	US-09-796-753-60	Sequence 60, Appl
556	6	1.2	133	9	US-09-738-626-6531	Sequence 6531, Ap	629	1.2	226	9	US-09-990-438-151	Sequence 151, App
557	6	1.2	135	10	US-09-864-761-36267	Sequence 36267, A	630	1.2	226	9	US-09-997-428-151	Sequence 151, App
558	6	1.2	136	10	US-09-833-017-23	Sequence 23, Appl	631	1.2	226	9	US-09-997-666-151	Sequence 151, App
559	6	1.2	137	10	US-09-925-301-1519	Sequence 1519, Ap	632	1.2	226	9	US-10-173-700-122	Sequence 122, App
560	6	1.2	143	10	US-09-867-550-1866	Sequence 1866, Ap	633	1.2	226	9	US-10-174-572-122	Sequence 122, App
561	6	1.2	147	9	US-10-091-504-1109	Sequence 1109, Ap	634	1.2	226	9	US-10-174-573-122	Sequence 122, App
562	6	1.2	147	10	US-09-764-869-1109	Sequence 1109, Ap	635	1.2	226	9	US-10-174-582-122	Sequence 122, App
563	6	1.2	148	9	US-09-975-4568-5	Sequence 5, Appl	636	1.2	226	9	US-10-174-588-122	Sequence 122, App
564	6	1.2	150	9	US-10-078-770-130	Sequence 130, App	637	1.2	226	9	US-10-175-739-122	Sequence 122, App
565	6	1.2	153	10	US-09-822-635-5	Sequence 5, Appl	638	1.2	226	9	US-10-175-740-122	Sequence 122, App
566	6	1.2	153	10	US-09-800-971-6	Sequence 6, Appl	639	1.2	226	9	US-10-175-743-122	Sequence 122, App
567	6	1.2	153	10	US-09-927-112-7	Sequence 7, Appl	640	1.2	226	9	US-10-176-492-122	Sequence 122, App
568	6	1.2	153	10	US-09-908-664-10	Sequence 10, Appl	641	1.2	226	9	US-10-176-488-122	Sequence 122, App
569	6	1.2	153	10	US-09-908-664-19	Sequence 19, Appl	642	1.2	226	9	US-10-176-747-122	Sequence 122, App
570	6	1.2	155	9	US-09-738-626-6458	Sequence 6458, Ap	643	1.2	226	9	US-10-176-750-122	Sequence 122, App
571	6	1.2	156	10	US-09-925-297-511	Sequence 511, App	644	1.2	226	9	US-10-176-985-122	Sequence 122, App
572	6	1.2	157	9	US-10-108-605-153	Sequence 153, App	645	1.2	226	9	US-10-176-987-122	Sequence 122, App
573	6	1.2	157	10	US-09-894-018-117	Sequence 117, App	646	1.2	226	9	US-10-176-992-122	Sequence 122, App
574	6	1.2	162	10	US-09-864-761-42286	Sequence 42286, A	647	1.2	226	9	US-10-176-993-122	Sequence 122, App
575	6	1.2	162	10	US-09-747-155-306	Sequence 306, App	648	1.2	226	9	US-10-184-658-122	Sequence 122, App
576	6	1.2	163	9	US-10-050-704-120	Sequence 120, App	649	1.2	226	9	US-09-990-711-151	Sequence 151, App
577	6	1.2	165	10	US-09-938-970-6	Sequence 6, Appl	650	1.2	226	9	US-10-173-695-122	Sequence 122, App
578	6	1.2	170	9	US-09-738-626-6851	Sequence 6851, Ap	651	1.2	226	9	US-10-173-697-122	Sequence 122, App
579	6	1.2	181	10	US-09-942-446-6	Sequence 6, Appl	652	1.2	226	9	US-10-173-705-122	Sequence 122, App
580	6	1.2	191	10	US-09-811-284-257	Sequence 257, App	653	1.2	226	9	US-10-174-576-122	Sequence 122, App
581	6	1.2	193	10	US-09-864-761-34864	Sequence 34864, A	654	1.2	226	9	US-10-174-585-122	Sequence 122, App
582	6	1.2	196	10	US-09-811-284-183	Sequence 183, Appl	655	1.2	226	9	US-10-174-586-122	Sequence 122, App
583	6	1.2	197	10	US-09-905-114-2	Sequence 2, Appl	656	1.2	226	9	US-10-175-747-122	Sequence 122, App
584	6	1.2	198	9	US-09-791-279-200	Sequence 200, App	657	1.2	226	9	US-10-176-481-122	Sequence 122, App
585	6	1.2	198	10	US-09-864-761-37569	Sequence 37569, A	658	1.2	226	9	US-10-176-485-122	Sequence 122, App
586	6	1.2	198	10	US-09-867-550-766	Sequence 766, App	659	1.2	226	9	US-10-176-487-122	Sequence 122, App
587	6	1.2	199	10	US-09-911-346-17	Sequence 17, Appl	660	1.2	226	9	US-10-176-493-122	Sequence 122, App
588	6	1.2	202	9	US-10-050-704-251	Sequence 251, App	661	1.2	226	9	US-10-176-756-122	Sequence 122, App
589	6	1.2	206	9	US-09-738-626-6923	Sequence 6923, Ap	662	1.2	226	9	US-10-176-911-122	Sequence 122, App
590	6	1.2	209	10	US-09-761-534A-12	Sequence 12, Appl	663	1.2	226	9	US-10-176-925-122	Sequence 122, App
591	6	1.2	210	10	US-09-761-534A-8	Sequence 8, Appl	664	1.2	226	9	US-10-176-978-122	Sequence 122, App
592	6	1.2	211	9	US-09-731-449-14	Sequence 14, Appl	665	1.2	226	9	US-10-179-510-122	Sequence 122, App
593	6	1.2	211	9	US-09-731-449-41	Sequence 41, Appl	666	1.2	226	9	US-10-180-543-122	Sequence 122, App
594	6	1.2	211	9	US-09-731-449-49	Sequence 49, Appl	667	1.2	226	9	US-10-180-544-122	Sequence 122, App
595	6	1.2	213	10	US-09-771-209-14	Sequence 14, Appl	668	1.2	226	9	US-10-180-546-122	Sequence 122, App
596	6	1.2	214	9	US-09-738-626-4579	Sequence 4579, Ap	669	1.2	226	9	US-10-180-547-122	Sequence 122, App
597	6	1.2	215	10	US-09-925-297-660	Sequence 660, App	670	1.2	226	9	US-10-180-549-122	Sequence 122, App
598	6	1.2	221	9	US-09-738-626-6107	Sequence 6107, Ap	671	1.2	226	9	US-10-180-555-122	Sequence 122, App
599	6	1.2	222	10	US-10-092-925-2	Sequence 2, Appl	672	1.2	226	9	US-10-180-559-122	Sequence 122, App
600	6	1.2	222	10	US-09-897-772-2	Sequence 8, Appl	673	1.2	226	9	US-10-181-000-122	Sequence 122, App
601	6	1.2	223	9	US-09-811-088-8	Sequence 19, Appl	674	1.2	226	9	US-10-183-010-122	Sequence 122, App
602	6	1.2	223	9	US-10-062-523-19	Sequence 1465, Ap	675	1.2	226	9		
603	6	1.2	224	10	US-09-764-864-1465		676	1.2	226	9		

969 6 1.2 226 9 US-10-206-912-122 Sequence 122, App
970 6 1.2 226 9 US-10-206-913-122 Sequence 122, App
971 6 1.2 226 9 US-10-206-914-122 Sequence 122, App
972 6 1.2 226 9 US-10-206-920-122 Sequence 122, App
973 6 1.2 226 9 US-10-206-921-122 Sequence 122, App
974 6 1.2 226 9 US-10-206-923-122 Sequence 122, App
975 6 1.2 226 9 US-10-206-925-122 Sequence 122, App
976 6 1.2 226 9 US-10-206-926-122 Sequence 122, App
977 6 1.2 226 9 US-10-206-927-122 Sequence 122, App
978 6 1.2 226 9 US-10-207-916-122 Sequence 122, App
979 6 1.2 226 9 US-10-207-917-122 Sequence 122, App
980 6 1.2 226 9 US-10-207-918-122 Sequence 122, App
981 6 1.2 226 9 US-10-207-919-122 Sequence 122, App
982 6 1.2 226 9 US-10-207-920-122 Sequence 122, App
983 6 1.2 226 9 US-10-207-925-122 Sequence 122, App
984 6 1.2 226 9 US-10-208-021-122 Sequence 122, App
985 6 1.2 226 9 US-10-208-022-122 Sequence 122, App
986 6 1.2 226 9 US-10-208-023-122 Sequence 122, App
987 6 1.2 226 9 US-10-208-026-122 Sequence 122, App
988 6 1.2 226 9 US-10-208-029-122 Sequence 122, App
989 6 1.2 226 9 US-10-208-030-122 Sequence 122, App
990 6 1.2 226 9 US-10-232-232-122 Sequence 122, App
991 6 1.2 226 9 US-09-990-427-151 Sequence 151, App
992 6 1.2 226 9 US-09-990-439-151 Sequence 151, App
993 6 1.2 226 9 US-10-173-693-122 Sequence 122, App
994 6 1.2 226 9 US-10-174-578-122 Sequence 122, App
995 6 1.2 226 9 US-10-175-741-122 Sequence 122, App
996 6 1.2 226 9 US-10-175-750-122 Sequence 122, App
997 6 1.2 226 9 US-10-176-986-122 Sequence 122, App
998 6 1.2 226 9 US-10-184-641-122 Sequence 122, App
999 6 1.2 226 9 US-10-187-888-122 Sequence 122, App
1000 6 1.2 226 10 US-09-990-456-151 Sequence 151, App

ALIGNMENTS

RESULT 1
US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match 54.2%; Score 271; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-247;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LAMDTLPDNRTRVEDNHNHYVSRLYCPSPHSHRELWVDVAEANRSQVKIHTILSNTRHQ 131
Db 1 LAMDTLPDNRTRVEDNHNHYVSRLYCPSPHSHRELWVDVAEANRSQVKIHTILSNTRHQ 60
QY 132 ASRWLVSDFPPFYGHPIRQITATGGFIEMGDVHRLMTATQVAPLMAFNPGYSDNST 191
Db 61 ASRWLVSDFPPFYGHPIRQITATGGFIEMGDVHRLMTATQVAPLMAFNPGYSDNST 120
QY 192 VVYFNGTVEVQWDHYVLOGWEDKGSFTFOALHHDGRIVEFAYKIPMSVPEISSQHP 251
Db 121 VVYFNGTVEVQWDHYVLOGWEDKGSFTFOALHHDGRIVEFAYKIPMSVPEISSQHP 180

QY 252 VKTCLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMSSAVEFTPLPTCLQHRSCD 311
Db 181 VKTCLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMSSAVEFTPLPTCLQHRSCD 240
QY 312 ACMSSDLTFNCSCWCHVLQRCSSGFDYRQEW 342
Db 241 ACMSSDLTFNCSCWCHVLQRCSSGFDYRQEW 271

RESULT 2
US-09-864-761-43750
; Sequence 43750, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weusheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43750
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004408.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EST_HUMAN HIT: AW028265.1, EVALUE 2.00e-26
OTHER INFORMATION: SWISSPROT HIT: Q09530, EVALUE 3.60e+00
US-09-864-761-43750

Query Match 10.6%; Score 53; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.3e-42; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0;
QY 27 HDEPGSGWAAGTGVGRNRRARESPCHVSEPDRTQSLDGGGTIAMDITLDP 79
Db 1 HDEPGSGWAAGTGVGRNRRARESPCHVSEPDRTQSLDGGGTIAMDITLDP 53

RESULT 3
US-09-867-550-198
Sequence 198, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-198

Query Match 2.0%; Score 10; DB 10; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 137 LSFDFPFYGH 146
Db 47 LSFDFPFYGH 56

RESULT 4
US-09-912-935-23
Sequence 23, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-23

Query Match 2.0%; Score 10; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 137 LSFDFPFYGH 146
Db 24 LSFDFPFYGH 33

RESULT 5
US-09-912-935-25
Sequence 25, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-25

Query Match 2.0%; Score 10; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 137 LSFDFPFYGH 146
Db 24 LSFDFPFYGH 33

RESULT 6
US-09-912-935-35
Sequence 35, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 425
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-35

Query Match 2.0%; Score 10; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.33; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 137 LSFDFPFYGH 146
Db 59 LSFDFPFYGH 68

RESULT 7
US-09-912-935-34
Sequence 34, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-34

Query Match 2.0%; Score 10; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-34

Query Match 2.0%; Score 10; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
|||||
Db 161 LSFDFPFYGH 170

RESULT 8

US-09-912-935-31
Sequence 31, Application US/09912935
Publication No. US2003002825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 499
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-31

Query Match 2.0%; Score 10; DB 9; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
|||||
Db 131 LSFDFPFYGH 140

RESULT 9

US-10-066-500-128
Sequence 128, Application US/10066500
Patent No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier

APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P31301C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/095998
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/097000
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/099601
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/145070

;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/149396
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 08/918874
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;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 09/114844
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: 09/136801
;; PRIOR FILING DATE: 1998-08-19
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;; PRIOR FILING DATE: 1998-08-19
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;; PRIOR APPLICATION NUMBER: 09/254311
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;; PRIOR FILING DATE: 2001-01-22
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/808689
;; PRIOR FILING DATE: 2001-03-14

;; PRIOR APPLICATION NUMBER: 09/866028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/870574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/886342
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: PCT/US98/14552
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US98/19093
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
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;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: PCT/US98/24855
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: 1998-12-01
;; PRIOR APPLICATION NUMBER: PCT/US98/25190
;; PRIOR FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

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Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146

Db 161 LSFDFPFYGH 170

RESULT 10

US-10-174-590-472

; Sequence 472, Application US/10174590

; Publication No. US20030008352A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC42

; CURRENT APPLICATION NUMBER: US/10/174,590

; CURRENT FILING DATE: 2002-06-18

; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-174-590-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 11

US-10-176-758-472

; Sequence 472, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-176-758-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 12

US-10-175-737-472

; Sequence 472, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 13

US-09-912-935-28

; Sequence 28, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 28
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-912-935-28

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 14

US-09-912-935-40

; Sequence 40, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 40
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-912-935-40

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

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RESULT 15
US-10-173-706-472
; Sequence 472, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-472

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Query Match      2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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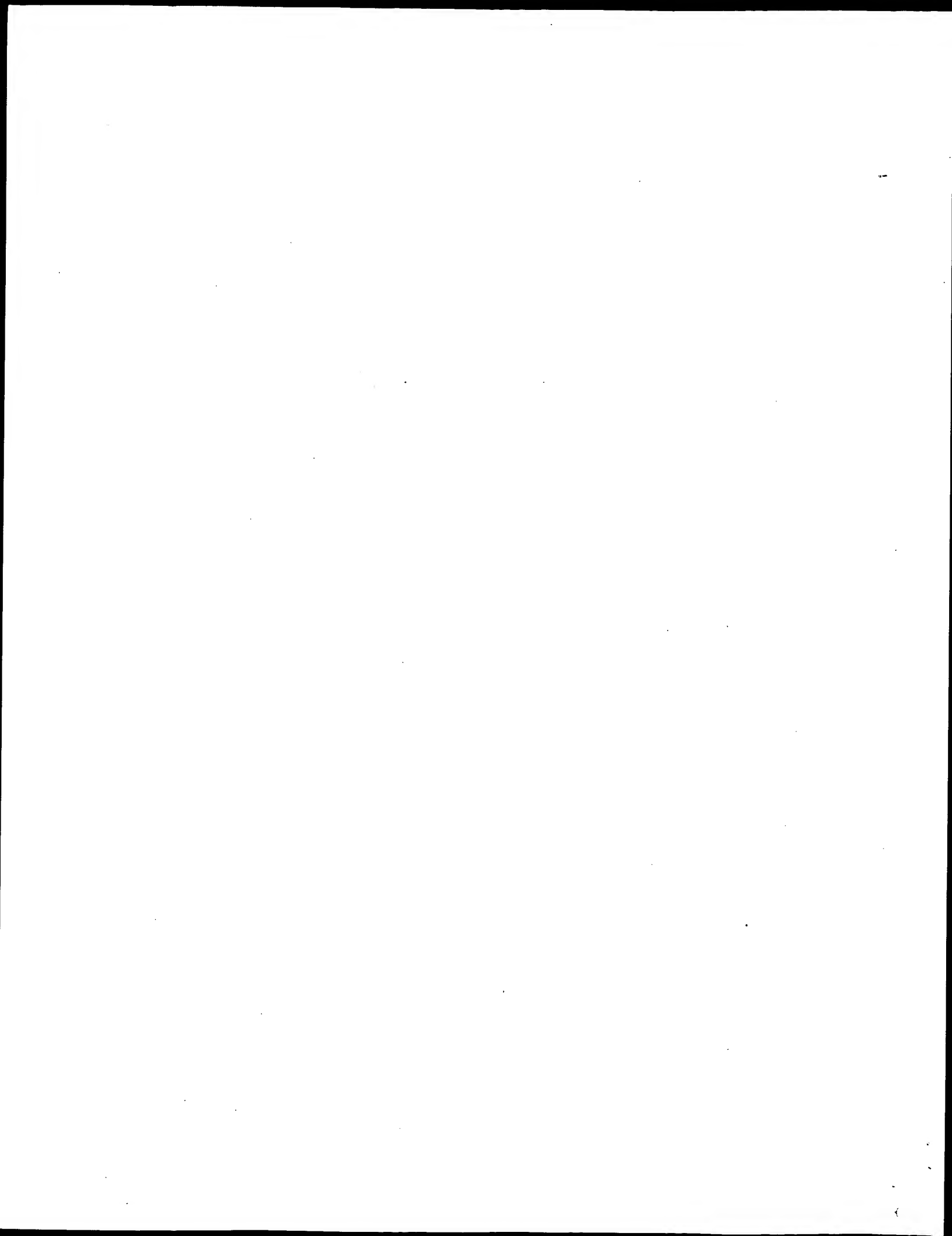
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Db 161 LSFDFPFYGH 170

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Search completed: April 22, 2003, 16:24:43
Job time : 43 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 16:06:40 ; Search time 322 Seconds
(without alignments)
1001.138 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 2691
Sequence: 1 MRGELWLVLVLRRAARALS.....YAEVEPSGHEKEGFMEAEQC 500

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2691	100.0	500	1 PCT-US01-24031-230
2	2691	100.0	500	1 PCT-US02-08253-230
3	2691	100.0	500	1 PCT-US02-29964-314
4	2691	100.0	500	23 US-09-918-715-230
5	2691	100.0	500	27 US-60-327-731-5
6	2691	100.0	500	27 US-60-327-731-15

7	2691	100.0	527	1	PCT-US02-29964-804	Sequence 804, App
8	2691	100.0	527	1	PCT-US02-29964-805	Sequence 805, App
9	2691	100.0	527	27	US-60-327-731-3	Sequence 3, Appli
10	2691	100.0	1002	1	PCT-US01-24031-179	Sequence 179, App
11	2691	100.0	1002	1	PCT-US02-08253-179	Sequence 179, App
12	2691	100.0	1002	23	US-09-918-715-179	Sequence 179, App
13	2607	96.9	488	1	PCT-US02-29964-315	Sequence 315, App
14	2607	96.9	488	27	US-60-327-731-10	Sequence 10, Appl
15	2604	96.8	482	27	US-60-327-731-8	Sequence 8, Appli
16	2566	95.4	502	1	PCT-US02-16639-5	Sequence 5, Appli
17	2566	95.4	502	25	US-10-156-487A-5	Sequence 12, Appl
18	2520	93.6	470	27	US-60-327-731-12	Sequence 12, App
19	2209	82.1	500	1	PCT-US01-24031-192	Sequence 192, App
20	2209	82.1	500	1	PCT-US01-24031-297	Sequence 297, App
21	2209	82.1	500	1	PCT-US02-08253-192	Sequence 192, App
22	2209	82.1	500	1	PCT-US02-08253-297	Sequence 297, App
23	2209	82.1	500	1	PCT-US02-16639-6	Sequence 6, Appli
24	2209	82.1	500	23	US-09-918-715-192	Sequence 192, App
25	2209	82.1	500	23	US-09-918-715-297	Sequence 297, App
26	2209	82.1	500	25	US-10-156-487A-6	Sequence 6, Appli
27	2185	81.2	431	1	PCT-US00-35260-36	Sequence 36, Appl
28	2185	81.2	431	23	US-09-912-935-36	Sequence 36, Appl
29	2185	81.2	431	25	US-10-168-365-36	Sequence 36, Appl
30	1296	48.2	528	27	US-60-242-679-1283	Sequence 1283, Ap
31	1295	48.1	435	27	US-60-327-731-14	Sequence 31, Appl
32	1295	48.1	499	1	PCT-US00-35260-31	Sequence 31, Appl
33	1295	48.1	499	23	US-09-912-935-31	Sequence 31, Appl
34	1295	48.1	499	25	US-10-168-365-31	Sequence 31, Appl
35	1295	48.1	529	1	PCT-US00-35260-28	Sequence 28, Appl
36	1295	48.1	529	1	PCT-US01-24031-189	Sequence 189, App
37	1295	48.1	529	1	PCT-US01-24031-200	Sequence 200, App
38	1295	48.1	529	1	PCT-US02-08253-189	Sequence 189, App
39	1295	48.1	529	1	PCT-US02-08253-200	Sequence 200, App
40	1295	48.1	529	1	PCT-US02-16639-4	Sequence 4, Appli
41	1295	48.1	529	23	US-09-912-935-28	Sequence 28, Appl
42	1295	48.1	529	23	US-09-912-935-40	Sequence 40, Appl
43	1295	48.1	529	23	US-09-918-715-189	Sequence 189, App
44	1295	48.1	529	23	US-09-918-715-200	Sequence 200, App
45	1295	48.1	529	25	US-10-156-487A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
PCT-US01-24031-230
; Sequence 230, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-24031-230

Query Match 100.0%; Score 2691; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGGAAKAGTVRGWNNRARESPGHVSEPD 60
QY 61 TQSQDLGGGTLMADTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTLMADTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
QY 301 LPTCLOHRSDDACMSDLTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAQEAEGRMCEDFQ 360
Db 301 LPTCLOHRSDDACMSDLTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAQEAEGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
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QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
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Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 2
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; Sequence 230, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOPHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-230

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Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TQSQDLGGGTLMADTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTLMADTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120

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QY 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
QY 301 LPTCLOHRSDDACMSDLTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAQEAEGRMCEDFQ 360
Db 301 LPTCLOHRSDDACMSDLTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAQEAEGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

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RESULT 3
PCT-US02-29964-314
; Sequence 314, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aildong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28

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; Remaining Prior Application data removed - See File Wrapper or PALM.
;
; NUMBER OF SEQ ID NOS: 992
;
; SOFTWARE: pt_FL_genes Version 6.0
;
; SEQ ID NO 314
;
; LENGTH: 500
;
; TYPE: PKT
;
; ORGANISM: Homo sapiens
;
PCT-US02-29964-314

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Query Match	100.0%;	Score	2691;	DB	1;	Length	500;
Best Local Similarity	100.0%;	Pred.	No. 7.9e-265;				
Matches	500;	Conservative	0;	Mismatches	0;	Indels	0; Gaps
QY	1	MRGELWLVLVLR	AARALSPQCAGHDEPGSGAAKGTVRGNRRRARES	CHVSEPD	R	60	
Db							
QY	1	MRGELWLVLVLR	AARALSPQCAGHDEPGSGAAKGTVRGNRRRARES	CHVSEPD	R	60	
Db							
QY	61	TQLSQDLGGTTLAMDTLPDNTRVVEDNHHSYYVSRLYPGPSEPHSRELWLDVAEANKRSVK	120				
Db							
QY	61	TQLSQDLGGTTLAMDTLPDNTRVVEDNHHSYYVSRLYPGPSEPHSRELWLDVAEANKRSVK	120				
Db							
QY	121	IHTILSNTHROASRVVLSFDPFFGHPLRQITTIATGGFIEMGDVIHRMLTATQIYVAPLMA	180				
Db							
QY	121	IHTILSNTHROASRVVLSFDPFFGHPLRQITTIATGGFIEMGDVIHRMLTATQIYVAPLMA	180				
Db							
QY	181	NENPGYSNDSTVVYFDNGCTVFVQMDHVYLQGWEDKGSETFOAALHHDGRIFPAYKEIPM	240				
Db							
QY	181	NENPGYSNDSTVVYFDNGCTVFVQMDHVYLQGWEDKGSETFOAALHHDGRIFPAYKEIPM	240				
Db							
QY	241	SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDOPSKVTSMSAVEFTP	300				
Db							
QY	241	SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDOPSKVTSMSAVEFTP	300				
Db							
QY	301	LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSGDFDRYOEWMDYCAQAEGRCMEDTQ	360				
Db							
QY	301	LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSGDFDRYOEWMDYCAQAEGRCMEDTQ	360				
Db							
QY	361	DEDHDSASPDTSFSYDGDLTTSSSLPIDSLLTDDOTKLNPYAGGDLGNLSPKTGCT	420				
Db							
QY	361	DEDHDSASPDTSFSYDGDLTTSSSLPIDSLLTDDOTKLNPYAGGDLGNLSPKTGCT	420				
Db							
QY	421	PVHLGTIGVILVALLVLAAILAGIYINGHPTSNAALFFIERPPHHWPAMKFRSHPDHST	480				
Db							
QY	421	PVHLGTIGVILVALLVLAAILAGIYINGHPTSNAALFFIERPPHHWPAMKFRSHPDHST	480				
Db							
QY	481	YAEVPSGHEKGFMEAEQC	500				
Db							
QY	481	YAEVPSGHEKGFMEAEQC	500				
Db							

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RESULT 4
US-09-918-715-230
; Sequence 230, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107_00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-918-715-230

Query Match	100.0%	Score 2691;	DB 23;	Length 500;
Best Local Similarity	100.0%	Pred. No.7.9e-265;		
Matches 500;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRGELWLLVLR	AAARALSPQAGHDEGPGSGWAARKGTVRGNRRRARESPGHVSE	PDR 60
DB	1	MRGELWLLVLR	AAARALSPQAGHDEGPGSGWAARKGTVRGNRRRARESPGHVSE	PDR 60
QY	61	TQLSQDLGGGT	LAMDITLPDNRTRVVDNHNHYSYVRLYGPSPHSEKELWVDVAE	ANRSQVK 120
DB	61	TQLSQDLGGGT	LAMDITLPDNRTRVVDNHNHYSYVRLYGPSPHSEKELWVDVAE	ANRSQVK 120
QY	121	IHTILSNTHROAS	RWVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAP	LMA 180
DB	121	IHTILSNTHROAS	RWVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAP	LMA 180
QY	181	NFNPGYSDNSTV	VYFDNGTSTVFVQWDHYVLQGWEDKGSFTFOAALHHDGRIVFAY	KEIPLM 240
DB	181	NFNPGYSDNSTV	VYFDNGTSTVFVQWDHYVLQGWEDKGSFTFOAALHHDGRIVFAY	KEIPLM 240
QY	241	SVPEISSQHPVK	TGLSDAFMLNPSDPVPSRRRESIFEYHRIELDPKVTSM	SAVETTP 300
DB	241	SVPEISSQHPVK	TGLSDAFMLNPSDPVPSRRRESIFEYHRIELDPKVTSM	SAVETTP 300
QY	301	LPTCLQHRSCD	CACWSSDLTFNCWCHVLQRCSSGFDRYRQEMDYGCAQAEGR	MCEDFQ 360
DB	301	LPTCLQHRSCD	CACWSSDLTFNCWCHVLQRCSSGFDRYRQEMDYGCAQAEGR	MCEDFQ 360
QY	361	DEDHDSAPDTS	FSFYDGLTITSSSLFIDSLTTEDYTKLPYAGDGLQNNLS	SPKTKGT 420
DB	361	DEDHDSAPDTS	FSFYDGLTITSSSLFIDSLTTEDYTKLPYAGDGLQNNLS	SPKTKGT 420
QY	421	PVHLGTIVGIV	LAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPAMKFRSH	PDHST 480
DB	421	PVHLGTIVGIV	LAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPAMKFRSH	PDHST 480
QY	481	YAEVEPSGHEK	EGFMEEAQC 500	
DB	481	YAEVEPSGHEK	EGFMEEAQC 500	
RESULT 5				
US-60-327-731-5				
; Sequence 5, Application US/60327731				
; GENERAL INFORMATION:				
; APPLICANT: Ghosh, Malabika				
; APPLICANT: Tang, Y. Tom				
; APPLICANT: Rep. Feiyan				
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factors				
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof				
; FILE REFERENCE: HYS-44				
; CURRENT APPLICATION NUMBER: US/60327,731				
; CURRENT FILING DATE: 2001-10-05				
; PRIOR APPLICATION NUMBER: PCT/US00/35017				
; PRIOR FILING DATE: 2000-12-22				
; PRIOR APPLICATION NUMBER: 09/552,317				
; PRIOR FILING DATE: 2000-04-25				
; PRIOR APPLICATION NUMBER: 09/486,725				
; PRIOR FILING DATE: 2000-01-21				
; NUMBER OF SEQ ID NOS: 15				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 5				
; LENGTH: 500				
; TYPE: PRT				
; ORGANISM: homo sapiens				
US-60-327-731-5				

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RESULT 5
US-60-327-731-5
; Sequence 5, Application US/60327731.5
;
; GENERAL INFORMATION:
;
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; TITLE OF INVENTION: Methods And Materials For The Preparation Of Polypeptides
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327-731-5
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/000000
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,343
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,747
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-5

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Query Match 100.0%; Score 2691; DB 27; Length 500;
 Best Local Similarity 100.0%; Pred. No. 7.9e+265;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
DB 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVEFTP 300
DB 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQCSGDFRYRQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQCSGDFRYRQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEHDHSDASPDTSFSPYDGLTSSSLFIDSLLTETDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 361 DEHDHSDASPDTSFSPYDGLTSSSLFIDSLLTETDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQ 500
DB 481 YAEVPSGHEKEGFMFAEQ 500

RESULT 6

US-60-327-731-15
; Sequence 15, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR FILING DATE: 2001-10-05
; CURRENT APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-15

Query Match 100.0%; Score 2691; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
DB 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120

DB 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITITATGGFIFMGDVIIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVEFTP 300
DB 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQCSGDFRYRQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQCSGDFRYRQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEHDHSDASPDTSFSPYDGLTSSSLFIDSLLTETDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 361 DEHDHSDASPDTSFSPYDGLTSSSLFIDSLLTETDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQ 500
DB 481 YAEVPSGHEKEGFMFAEQ 500

RESULT 7

PCT-US02-29964-804
; Sequence 804, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05

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; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 805
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-805

Query Match      100.0%; Score 2691; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 8,6e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 60
Db 28 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 87
Qy 61 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 88 TQLSODLGGGTAMDITLDPNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 147
Qy 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 180
Db 148 IHTILSNTHROASRVLSFDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 207
Qy 181 NFNPGYSDNSTVYVFDNGTVFVQWDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 208 NFNPGYSDNSTVYVFDNGTVFVQWDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 267
Qy 241 SVPEISSQHPVKITGLSDAFMILNPSDPVPESRRRSIFEYHRIELDP SKVTSMSAVEFTP 300
Db 268 SVPEISSQHPVKITGLSDAFMILNPSDPVPESRRRSIFEYHRIELDP SKVTSMSAVEFTP 327
Qy 301 LPTCLOHRSQCDACMSDDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDEQ 360
Db 328 LPTCLOHRSQCDACMSDDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDEQ 387
Qy 361 DEHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 388 DEHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 447
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
Qy 481 YAEVEPSGHEKEGFMEEAEOC 500
Db 508 YAEVEPSGHEKEGFMEEAEOC 527

RESULT 8
PCT-US02-29964-805
; Sequence 805, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
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RESULT 9

US-60-327-731-3
; Sequence 3, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 527
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-3

Query Match 100.0%; Score 2691; DB 27; Length 527;
Best Local Similarity 100.0%; Pred. No. 8.6e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRGELWLLVLR	EAARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD	60
Db	28	MRGELWLLVLR	EAARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD	87
QY	61	TQLSQDLGGGT	LAMDTPDNTRRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK	120
Db	88	TQLSQDLGGGT	LAMDTPDNTRRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK	147
QY	121	IHTILSNTHRO	ASRVVLSDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAPLMA	180
Db	148	IHTILSNTHRO	ASRVVLSDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAPLMA	207
QY	181	NFNPYSDNST	VVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	240
Db	208	NFNPYSDNST	VVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	267
QY	241	SVPEISSQHP	VKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	300
Db	268	SVPEISSQHP	VKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	327
QY	301	LPTCLOHRS	CDACMSDLTFNCWCHVLQRCSSGFDRIQEWMDYGCQAEGRMCEDFQ	360
Db	328	LPTCLOHRS	CDACMSDLTFNCWCHVLQRCSSGFDRIQEWMDYGCQAEGRMCEDFQ	387
QY	361	DEHDASPD	TSRSPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	420
Db	388	DEHDASPD	TSRSPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	447
QY	421	PVHLGTIV	IGVILVALLVAAILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHST	480
Db	448	PVHLGTIV	IGVILVALLVAAILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHST	507
QY	481	YAEVPSG	HEKEGFMEAEQC 500	
Db	508	YAEVPSG	HEKEGFMEAEQC 527	

RESULT 10

PCT-US01-24031-179
; Sequence 179, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein

; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-24031-179

Query Match 100.0%; Score 2691; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.4e-264;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRGELWLLVLR	EAARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD	60
Db	503	MRGELWLLVLR	EAARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPD	562
QY	61	TQLSQDLGGGT	LAMDTPDNTRRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK	120
Db	563	TQLSQDLGGGT	LAMDTPDNTRRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK	622
QY	121	IHTILSNTHRO	ASRVVLSDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAPLMA	180
Db	623	IHTILSNTHRO	ASRVVLSDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQYVAPLMA	682
QY	181	NFNPYSDNST	VVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	240
Db	683	NFNPYSDNST	VVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	742
QY	241	SVPEISSQHP	VKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	300
Db	743	SVPEISSQHP	VKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	802
QY	301	LPTCLOHRS	CDACMSDLTFNCWCHVLQRCSSGFDRIQEWMDYGCQAEGRMCEDFQ	360
Db	803	LPTCLOHRS	CDACMSDLTFNCWCHVLQRCSSGFDRIQEWMDYGCQAEGRMCEDFQ	862
QY	361	DEHDASPD	TSRSPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	420
Db	863	DEHDASPD	TSRSPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	922
QY	421	PVHLGTIV	IGVILVALLVAAILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHST	480
Db	923	PVHLGTIV	IGVILVALLVAAILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHST	982
QY	481	YAEVPSG	HEKEGFMEAEQC 500	
Db	983	YAEVPSG	HEKEGFMEAEQC 1002	

RESULT 11

PCT-US02-08253-179
; Sequence 179, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850

; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-179

Query Match 100.0%; Score 2691; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.4e-264;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARSPGHVSEPD 60
DB 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARSPGHVSEPD 562
QY 61 TQSQDLGGGTAMDLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
DB 563 TQSQDLGGGTAMDLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 622
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 682
QY 181 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
QY 241 SVPEISSQHPVKTGSLDAFMIINSPDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
DB 743 SVPEISSQHPVKTGSLDAFMIINSPDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 802
QY 301 LPTCLQHRSCDACMSDITFNCWSCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDITFNCWSCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPTSFSPYDGLTTSLSLFDISLTEDDTKLPYAGDGLQNNLSPKTKGT 420
DB 863 DEDHDSASPTSFSPYDGLTTSLSLFDISLTEDDTKLPYAGDGLQNNLSPKTKGT 922
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 480
DB 923 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMEEAQC 500
DB 983 YAEVPSGHEKEGFMEEAQC 1002

RESULT 12
US-09-918-715-179
; Sequence 179, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179
Query Match 100.0%; Score 2691; DB 23; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.4e-264;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARSPGHVSEPD 60
DB 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRARSPGHVSEPD 562
QY 61 TQSQDLGGGTAMDLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
DB 563 TQSQDLGGGTAMDLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 622
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 682
QY 181 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
QY 241 SVPEISSQHPVKTGSLDAFMIINSPDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
DB 743 SVPEISSQHPVKTGSLDAFMIINSPDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 802
QY 301 LPTCLQHRSCDACMSDITFNCWSCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDITFNCWSCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPTSFSPYDGLTTSLSLFDISLTEDDTKLPYAGDGLQNNLSPKTKGT 420
DB 863 DEDHDSASPTSFSPYDGLTTSLSLFDISLTEDDTKLPYAGDGLQNNLSPKTKGT 922
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 480
DB 923 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMEEAQC 500
DB 983 YAEVPSGHEKEGFMEEAQC 1002
RESULT 13
PCT-US02-29964-315
; Sequence 315, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aigong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 315
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-315

Query Match 96.9%; Score 2607; DB 1; Length 488;
Best Local Similarity 97.6%; Pred. No. 2.9e-256;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60

QY 61 TQSQDLGGGTAMDTPDNTRVVDENHNSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
DB 61 TQSQDLGGGTAMDTPDNTRVVDENHNSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120

QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180

QY 181 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEVETP 300
DB 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEVETP 300

QY 301 LPTCLQHRSCDACSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360

QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGT 420
DB 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGT 420

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480

QY 481 YAEVPSGHEKEGFMEEAQC 500
DB 469 YAEVPSGHEKEGFMEEAQC 488

RESULT 14
US-60-327-731-10
; Sequence 10, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017

; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-10

Query Match 96.9%; Score 2607; DB 27; Length 488;
Best Local Similarity 97.6%; Pred. No. 2.9e-256;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60

QY 61 TQSQDLGGGTAMDTPDNTRVVDENHNSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
DB 61 TQSQDLGGGTAMDTPDNTRVVDENHNSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120

QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180

QY 181 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEVETP 300
DB 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEVETP 300

QY 301 LPTCLQHRSCDACSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360

QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGT 420
DB 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGT 420

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480

QY 481 YAEVPSGHEKEGFMEEAQC 500
DB 469 YAEVPSGHEKEGFMEEAQC 488

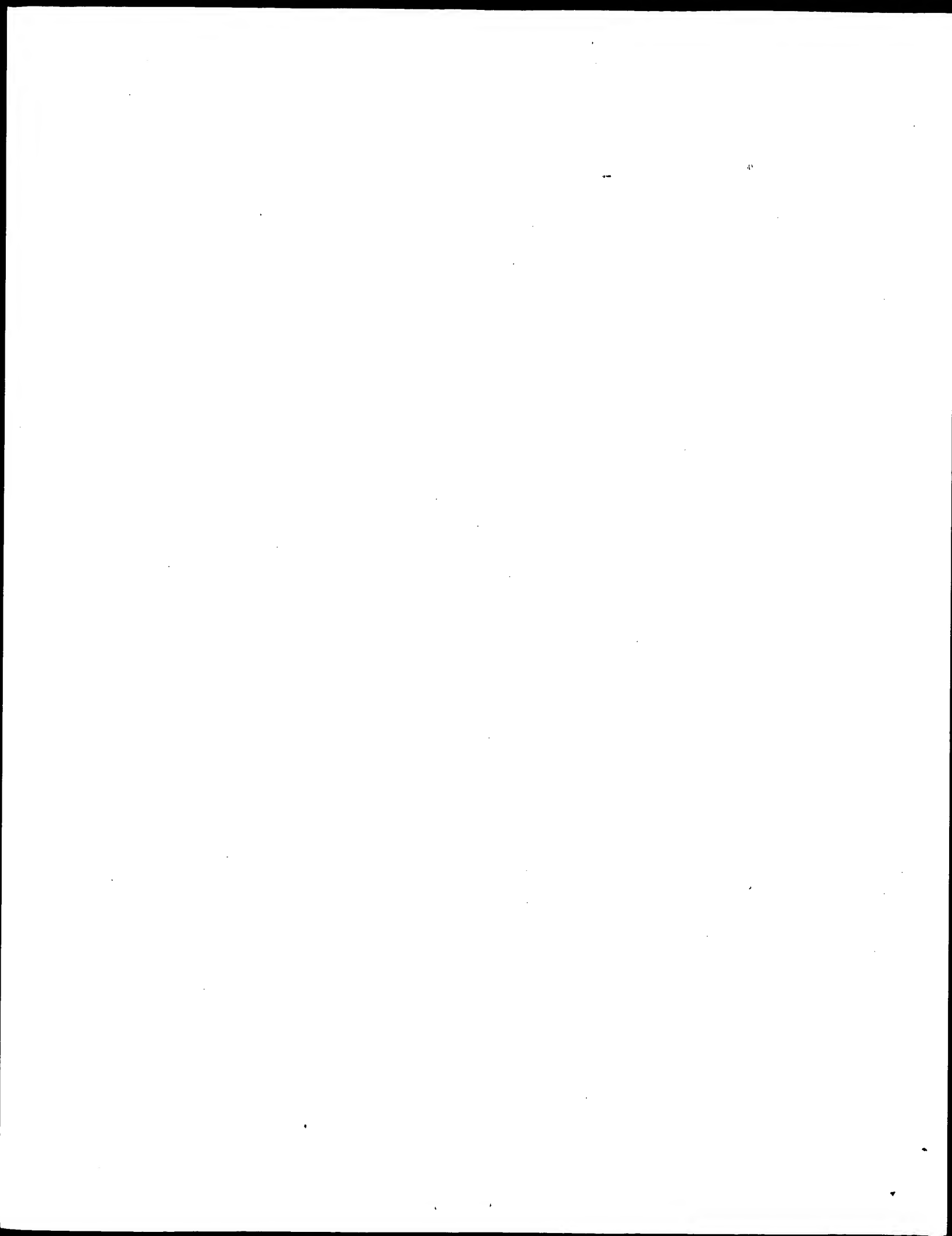
RESULT 15
US-60-327-731-8
; Sequence 8, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 482
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-60-327-731-8

Query Match 96.8%; Score 2604; DB 27; Length 482;
Best Local Similarity 100.0%; Pred. No. 5,7e-256;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	LSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP	78
Db	1	LSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP	60
QY	79	DNRTRVEDNHSYYYSRLYGPSEPHSRELWVDVAEANKSOVKIHTILSNTHRQASRVVLS	138
Db	61	DNRTRVEDNHSYYYSRLYGPSEPHSRELWVDVAEANKSQVKIHTILSNTHRQASRVVLS	120
QY	139	FDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMAENFPGYSDNSTVYFDNG	198
Db	121	FDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMAENFPGYSDNSTVYFDNG	180
QY	199	TVFVVQWDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSD	258
Db	181	TVFVVQWDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSD	240
QY	259	AFMILNPSPDVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSDDL	318
Db	241	AFMILNPSPDVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSDDL	300
QY	319	TENCSCWHLQRCSSGFDRYRQEWMDYGCQAQEAEGRMCEDFODEDHSASPDTSFSPYDG	378
Db	301	TENCSCWHLQRCSSGFDRYRQEWMDYGCQAQEAEGRMCEDFODEDHSASPDTSFSPYDG	360
QY	379	DLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA	438
Db	361	DLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA	420
QY	439	AIILAGIYINGHPTNAALFFIERPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMEAE	498
Db	421	AIILAGIYINGHPTNAALFFIERPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMEAE	480
QY	499	QC 500	
Db	481	QC 482	

Search completed: April 22, 2003, 16:14:10
Job time : 326 secs



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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:07:15 ; Search time 36 Seconds
(without alignments)
2191.561 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLRRAALSL.....YAEVPSGHEKEGFMEAEQC 500

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 718614 seqs, 157792391 residues

Total number of hits satisfying chosen parameters: 718614

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2691	100.0	500	6	US-10-266-252-5	Sequence 5, Appli
2	2691	100.0	500	6	US-10-266-252-15	Sequence 15, Appl
3	2691	100.0	500	7	US-60-453-135-13631	Sequence 13631, A
4	2691	100.0	500	7	US-60-453-050-13631	Sequence 13631, A
5	2691	100.0	527	6	US-10-266-252-3	Sequence 3, Appli
6	2607	96.9	488	6	US-10-266-252-10	Sequence 10, Appl
7	2604	96.8	482	6	US-10-266-252-8	Sequence 8, Appli
8	2520	93.6	470	6	US-10-266-252-12	Sequence 12, Appl
9	2302	85.5	427	7	US-60-453-135-13630	Sequence 13630, A
10	2302	85.5	427	7	US-60-453-050-13630	Sequence 13630, A
11	2007	74.6	400	6	US-10-218-140-5790	Sequence 5790, Ap
12	1295	48.1	435	6	US-10-266-252-14	Sequence 14, Appl
13	1294	48.1	529	6	US-10-123-923A-472	Sequence 472, App
14	1294	48.1	529	6	US-10-205-892-472	Sequence 472, App
15	1294	48.1	529	6	US-10-174-575-472	Sequence 472, App
16	1294	48.1	529	6	US-10-174-575A-472	Sequence 472, App
17	1294	48.1	529	6	US-10-187-755-472	Sequence 472, App
18	1294	48.1	529	6	US-10-187-749-472	Sequence 472, App
19	1294	48.1	529	6	US-10-199-672-472	Sequence 472, App
20	1294	48.1	529	6	US-10-194-486-472	Sequence 472, App
21	1275.5	47.4	530	1	PCT-US02-34451-12	Sequence 12, Appl
22	1275.5	47.4	530	6	US-10-281-478-12	Sequence 12, Appl
23	1150	42.7	379	7	US-60-452-680-20245	Sequence 20245, A
24	697	25.9	146	6	US-10-264-237-2453	Sequence 2453, Ap
25	682.5	25.4	290	6	US-10-218-140-526	Sequence 526, App
26	115.5	4.3	1265	5	US-09-724-676-82419	Sequence 82419, A

ALIGNMENTS

RESULT 1

US-10-266-252-5

: Sequence 5, Application US/10266252

: GENERAL INFORMATION:

: APPLICANT: Ghosh, Malabika

: APPLICANT: Tang, Y. Tom

: TITLE OF INVENTION: Ren, Feiyan

: TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like

: FILE REFERENCE: HVS-44A

: CURRENT APPLICATION NUMBER: US/10/266,252

: CURRENT FILING DATE: 2002-10-07

: PRIOR APPLICATION NUMBER: 60/327,731

: PRIOR FILING DATE: 2001-10-05

: PRIOR APPLICATION NUMBER: PCT/US00/35017

: PRIOR FILING DATE: 2000-12-22

: PRIOR APPLICATION NUMBER: 09/552,317

: PRIOR FILING DATE: 2000-04-25

: PRIOR APPLICATION NUMBER: 09/488,725

: PRIOR FILING DATE: 2000-01-21

: NUMBER OF SEQ ID NOS: 15

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 5

: LENGTH: 500

: TYPE: PRT

: ORGANISM: homo sapiens

: US-10-266-252-5

Query Match 100.0%; Score 2691; DB 6; Length 500;

Best Local Similarity 100.0%; Pred. No. 1.8e+226; Indels 0; Gaps 0;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAGTGVGRNRRRARESPGHVSEPD 60

Db 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAGTGVGRNRRRARESPGHVSEPD 60

Qy 61 TQSLQDLGGGTLMADTLPDNRTRVVDNHNHYSYVRLXGSPHRELWVDVAEANSQVK 120

Db 61 TQSLQDLGGGTLMADTLPDNRTRVVDNHNHYSYVRLXGSPHRELWVDVAEANSQVK 120

Qy 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180

Db 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180

Qy 181 NFNPYSDNSVTVYFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Db 181 NFNPYSDNSVTVYFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPSPKVTSMVAEFTP 300

Sequence 82419, A

Sequence 82416, A

Sequence 82417, A

Sequence 82418, A

Sequence 82415, A

Sequence 82412, A

Db 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 2

US-10-266-252-15
; Sequence 15, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HVS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-15

Query Match 100.0%; Score 2691; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSDQLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSDQLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVLSFDFFPGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVLSFDFFPGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

Db 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 3

US-60-453-135-13631
; Sequence 13631, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13631

Query Match 100.0%; Score 2691; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSDQLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSDQLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVLSFDFFPGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVLSFDFFPGHPLRQITATGGIFMGDVIRHMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGCACQAEAGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALEFFIERPHHPWPAKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 4

US-60-453-050-13631
; Sequence 13631, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453.050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13631

Query Match 100.0%; Score 2691; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGHAAKCTVGRNRRRARESPGHVSEPD 60
|||||
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGHAAKCTVGRNRRRARESPGHVSEPD 60
|||||

QY 61 TQLSODLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
Db 61 TQLSODLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||

QY 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||
Db 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||

QY 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||
Db 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||

QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
|||||
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
|||||

QY 301 LPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360
|||||
Db 301 LPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360
|||||

QY 361 DEHDHSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||
Db 361 DEHDHSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||

QY 481 YAEVPSGHEKEGMEAEQC 500
|||||
Db 481 YAEVPSGHEKEGMEAEQC 500
|||||

RESULT 5

US-10-266-252-3
; Sequence 3, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A

; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 527
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-3

Query Match 100.0%; Score 2691; DB 6; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.9e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGHAAKCTVGRNRRRARESPGHVSEPD 60
|||||
Db 28 MRGELWLLVLRARALSPQAGHDEGPGSGHAAKCTVGRNRRRARESPGHVSEPD 87
|||||

QY 61 TQLSODLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
Db 88 TQLSODLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 147
|||||

QY 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||
Db 148 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 207
|||||

QY 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||
Db 208 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 267
|||||

QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
|||||
Db 268 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 327
|||||

QY 301 LPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360
|||||
Db 328 LPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 387
|||||

QY 361 DEHDHSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||
Db 388 DEHDHSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 447
|||||

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||
Db 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
|||||

QY 481 YAEVPSGHEKEGMEAEQC 500
|||||
Db 508 YAEVPSGHEKEGMEAEQC 527
|||||

RESULT 6

US-10-266-252-10
; Sequence 10, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-10

Query Match 96.9%; Score 2607; DB 6; Length 488;
Best Local Similarity 97.6%; Pred. No. 3.7e-219;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60

QY 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
Db 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120

QY 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180

QY 181 NFNPYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAKELPM 240
Db 181 NFNPYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAKELPM 240

QY 241 SVPEISSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300

QY 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMWDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMWDYGAQAEGRMCEDFQ 360

QY 361 DEHDHSDPSTSFSDYDGLTTSSSLFIDSLTTE-----GLQNNLSPKTKGT 420
Db 361 DEHDHSDPSTSFSDYDGLTTSSSLFIDSLTTE-----GLQNNLSPKTKGT 408

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDST 480
Db 409 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDST 468

QY 481 YAEVPSGHEKEGMEAEQC 500
Db 469 YAEVPSGHEKEGMEAEQC 488

RESULT 7
US-10-266-252-8
; Sequence 8, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HVS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-8

Query Match 96.8%; Score 2604; DB 6; Length 482;
Best Local Similarity 100.0%; Pred. No. 6.7e-219;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSODLGGGTLMADTLP 78
Db 1 LSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSODLGGGTLMADTLP 60

QY 79 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 138
Db 61 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 120

QY 139 FDPFFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 198
Db 121 FDPFFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 180

QY 199 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAKELPMSPVPEISSOHPVKTGLSD 258
Db 181 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAKELPMSPVPEISSOHPVKTGLSD 240

QY 259 AFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDDL 318
Db 241 AFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDDL 300

QY 319 TFNCWCHVLQRCSSGFDYRQEMWDYGAQAEGRMCEDFQDEHDSASPTSFSPYDG 378
Db 301 TFNCWCHVLQRCSSGFDYRQEMWDYGAQAEGRMCEDFQDEHDSASPTSFSPYDG 360

QY 379 DLTTSSSLFIDSLTTEDEDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 438
Db 361 DLTTSSSLFIDSLTTEDEDTKLNYPYAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 420

QY 439 AITLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDSTYAEVPSGHEKEGMEAE 498
Db 421 AITLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDSTYAEVPSGHEKEGMEAE 480

QY 499 QC 500
Db 481 QC 482

RESULT 8
US-10-266-252-12
; Sequence 12, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HVS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1

QY 374 SPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTVPVHLGTIVGIVLA 433
Db 301 SPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTVPVHLGTIVGIVLA 360
QY 434 VLLVAAIILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEVPPSGHEKEG 493
Db 361 VLLVAAIILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEVPPSGHEKEG 420
QY 494 FMEAEQC 500
Db 421 FMEAEQC 427

RESULT 11
US-10-218-140-5790
; Sequence 5790, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; PRIOR FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 1999-04-05
; PRIOR FILING DATE: 1999-04-02
; PRIOR FILING DATE: 1999-04-02
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curator Version 1.0
; SEQ ID NO 5790
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: "Xaa" = "Any Amino Acid"
US-10-218-140-5790

Query Match 74.6%; Score 2007; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.8e-167;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD 60
Db 29 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD 88
QY 61 TQSLDGLGGTILAMDTLPDNRTRVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 89 TQSLDGLGGTILAMDTLPDNRTRVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 148
QY 121 IHTILSNTHRCASRVLSDFEPFYGHPLRQITATGTFIMGDVIHRMLTATQYVAPLMA 180
Db 149 IHTILSNTHRCASRVLSDFEPFYGHPLRQITATGTFIMGDVIHRMLTATQYVAPLMA 208
QY 181 NFNGYSDNSTVYVFDNGTFVQVQWHDVYLQGWEDKGSFTFOAALHHDGRIVFAYPEIM 240
Db 209 NFNGYSDNSTVYVFDNGTFVQVQWHDVYLQGWEDKGSFTFOAALHHDGRIVFAYPEIM 268
QY 241 SVPEISSQHPVKTGLSDAFMLNPSFDPVPSRRSIFFYHRIELDP SKVTSMAVEFTP 300
Db 269 SVPEISSQHPVKTGLSDAFMLNPSFDPVPSRRSIFFYHRIELDP SKVTSMAVEFTP 328
QY 301 LPTCLQHRSCDACMSSDLTFNCMCHVLRQCSGFDRIYRWMDYGCQAEGRMCEDFQ 360
Db 329 LPTCLQHRSCDACMSSDLTFNCMCHVLRQCSGFDRIYRWMDYGCQAEGRMCEDFQ 388
QY 361 DEDHDSASPD 371

Db 389 DEDHDSASPD 399

RESULT 12
US-10-266-252-14
; Sequence 14, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 435
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-14

Query Match 48.1%; Score 1295; DB 6; Length 435;
Best Local Similarity 57.3%; Pred. No. 1.5e-104;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVED-NHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHR 130
Db 1 LLLDGDQDNNTEEDTDHNYIISRIYSPDSASRDLMWYNDQMEKDKVKIHGILSNTHR 60
QY 131 QASRVVLSDFEPFYGHPLRQITATGTFIMGDVIHRMLTATQYVAPLMAFNPVSDNS 190
Db 61 QARVNLSDFFEPFYGHFLREITVATCGFIYGEVHRLTATQYIAPLMANFDPVSRSNS 120
QY 191 TVYFONGTVFVQWHDVYLQGWEDKGSFTFOAALHHDGRIVFAYPEIMSVPEISSQH 250
Db 121 TVYFONGTVFVQWHDVYLQGWEDKGSFTFOAALHHDGRIVFAYPEIMSVPEISSQH 180
QY 251 PVKTVGLSDAFMLNPSFDPVPSRRSIFFYHRIELDP SKVTSMAVEFTP LPTCLQHRSC 310
Db 181 PVKTVGLSDAFMLNPSFDPVPSRRSIFFYHRIELDP SKVTSMAVEFTP LPTCLQHRSC 240
QY 311 DACMSDLTFNCMCHVLRQCSGFDRIYRWMDYGCQAEGRMCEDFODHDSASPD 370
Db 241 GPCVSSQIGFNCMCHVLRQCSGFDRIYRWMDYGCQAEGRMCEDFODHDSASPD 300
QY 371 T--SFSYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTIVGIVLA 424
Db 301 TIGATTQPRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNAGSTDDSAAEKKGSTLHA 360
QY 425 GTIVGTVLAVLVAAILAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 361 GLIVGLLILVLAIVTAVILVYVYHHTTSAASIFFIERRPSRWPMKFRSGHGPAYAEV 420
QY 485 EPSGHEKEGMEAEQC 500
Db 421 EPVG-EKEGFIYSEQC 435

RESULT 13
US-10-125-923A-472
; Sequence 472, Application US/10125923A
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Pan, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-923A-472
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Query Match 48.1%; Score 1294; DB 6; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.5e-104;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSRELWVDVAEANRSQVKIHTILSNTHR 130
DB 95 LLLDDGQDNNTQIEDTDHNYIYSRIYGPSPDSASRDLVWVDQEKDKVKGILSNTHR 154
QY 131 QASRVVLSDFPFYGHPLRQITATGGIFMGDVHRLMTATQVYAPLMANFPGYSDNS 190
DB 155 QAARVNLSDPFYGHFLREITVATGGFIYGEVYHRLMTATQVYAPLMANFDPVSRSNS 214
QY 191 TVVYFDNGTVFVQVMDHYVLOGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 250
DB 215 TVRYFDNGTALVQVMDHYVLOGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 274
QY 251 PVKTLGLSDAFMLNPSDPVPSRRSIFEFYHRIELDPKSVTSMASAVEFTPLPTCLQHRSC 310
DB 275 PVKGLSDAFVVRHRIQIPNVRRTIYEHYHRLVQMSKITNISAVEMTPTCLQFNRC 334
QY 311 DACMSSDLTFNGSWCHVLRQSSGDRYRQEMDYGCQAEGRCNCEQFQEDHDHSDASPD 370
DB 335 GPCVSSQIGFNGSWCSKLRQSSGDRYRQEMDYGCQAEGRCNCEQFQEDHDHSDASPD 394
QY 371 T--SFPYDGLTTS--SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPTVHL 424
DB 395 TVGATQTQRLVLTTRAVTSQFPLPTEDDTKALHLKDKNGASTDSSAEKKGGLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFTIERRPHHPAMKFRSHDPHSTYAEV 484
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DB 455 GLIIGILVILVATAILVTVYMYHHPTSAASIFFIERRPSRWPAKFRRGSGHPAYAEV 514
QY 485 EFSGHEKEGFMDEAQC 500
DB 515 EPVG-EKEGFIIVSEQ 529

RESULT 14
US-10-205-892-472
; Sequence 472, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC517
; CURRENT APPLICATION NUMBER: US/10/205,892
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-892-472
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Query Match 48.1%; Score 1294; DB 6; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.5e-104;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSRELWVDVAEANRSQVKIHTILSNTHR 130
DB 95 LLLDDGQDNNTQIEDTDHNYIYSRIYGPSPDSASRDLVWVDQEKDKVKGILSNTHR 154
QY 131 QASRVVLSDFPFYGHPLRQITATGGIFMGDVHRLMTATQVYAPLMANFPGYSDNS 190
DB 155 QAARVNLSDPFYGHFLREITVATGGFIYGEVYHRLMTATQVYAPLMANFDPVSRSNS 214
QY 191 TVVYFDNGTVFVQVMDHYVLOGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 250
DB 215 TVRYFDNGTALVQVMDHYVLOGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 274
QY 251 PVKTLGLSDAFMLNPSDPVPSRRSIFEFYHRIELDPKSVTSMASAVEFTPLPTCLQHRSC 310
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Db 275 PKVGLSDAFVWVHRIQQIPNVRRRTIYEHVLELQMSKITNISAVEMTPTCLQFNRC 334
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Db 335 GPCVSSQIGFNCSSWCKLQRCSSGDFRHRQDWVDSGCPFEESKEKMCENTPEVETSSRTTT 394
QY 371 T--SFSPYDGLTTS---SSLFIDSITTEDDTKLNYPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTTQFRLVLTTRAVTSQPTSLPTEDDTKIALHLKONGASTDDSAEKKGGTLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPAKFRSHPDHSTYAEV 484
Db 455 GLIIGILILVIVATAILVTVYVYHHPTSAASIFFIERRPSRWPAMKFRGSGHPAYAEV 514
QY 485 EPSGHEKEGFMEEQC 500
Db 515 EPVG-EKEGFIVSEQ 529

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RESULT 15

US-10-174-575-472

; Sequence 472, Application US/10174575

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C35

; CURRENT APPLICATION NUMBER: US/10/174,575

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-174-575-472

Query Match

48.1%; Score 1294; DB 6; Length 529;

Best Local Similarity 57.1%; Pred. No. 2.5e-104;

Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

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QY 72 LAMDTLPDNRTRVED-NHSYVYVSRLYGPFSEPHSRELWVDVAEANKRSQVKIHTILSNTHR 130

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Db 95 LLLDDGQDNNTQIEDTDHNYISRIYGPSSASRDLWVNIQNEKDKVKIHGILSNTHR 154
QY 131 QASRVLSFDFPFYGHPLRQITATGFIIPMGDVIHRLMTATQYVAPLMAFNPNPGYSDNS 190
Db 155 QAARVNLSEDFPFYGHPLREITVATGFIIVTGEVHRLMTATQYIAPLMAFNPDPSYRNS 214
QY 191 TVVYFDNGTVFVWVDHVVYLGQWEDKCSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVVWVDHVVHLDQNYNLGSGFTFOATLLMDGRIFIEGYKEIPVLVQTQISSTNH 274
QY 251 PVKTGLSDAFMILNPSDPVPESRRRSIFEXHRIELDPKSVTSMASAVEFTPLPTCLQHRSC 310
Db 275 PKVGLSDAFVWVHRIQQIPNVRRRTIYEHVLELQMSKITNISAVEMTPTCLQFNRC 334
QY 311 DACMSSDLTFNCSSCHVLCRCSSGDFRYQEWMDYGCQAQEAERGMCEDFODEDHDSASPD 370
Db 335 GPCVSSQIGFNCSSWCKLQRCSSGDFRHRQDWVDSGCPFEESKEKMCENTPEVETSSRTTT 394
QY 371 T--SFSPYDGLTTS---SSLFIDSITTEDDTKLNYPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTTQFRLVLTTRAVTSQPTSLPTEDDTKIALHLKONGASTDDSAEKKGGTLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPAKFRSHPDHSTYAEV 484
Db 455 GLIIGILILVIVATAILVTVYVYHHPTSAASIFFIERRPSRWPAMKFRGSGHPAYAEV 514
QY 485 EPSGHEKEGFMEEQC 500
Db 515 EPVG-EKEGFIVSEQ 529

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Job time : 39 secs

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 15:16:56 ; Search time 146 Seconds
(without alignments)

2207.990 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

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Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending Patents_AA_Main:*

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
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24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	500	100.0	500	1	PCT-US02-08253-230
3	500	100.0	500	1	PCT-US02-29964-314
4	500	100.0	500	23	US-09-918-715-230
5	500	100.0	500	27	US-60-327-731-5
6	500	100.0	500	27	US-60-327-731-15
					Sequence 230, App
					Sequence 230, App
					Sequence 314, App
					Sequence 230, App
					Sequence 5, Appli
					Sequence 15, Appli

500	100.0	527	1	PCT-US02-29964-804	Sequence 804, App
500	100.0	527	1	PCT-US02-29964-805	Sequence 805, App
500	100.0	527	27	US-60-327-731-3	Sequence 3, Appli
500	100.0	1002	1	PCT-US01-24031-179	Sequence 179, App
500	100.0	1002	1	PCT-US02-08253-179	Sequence 179, App
500	100.0	1002	23	US-09-918-715-179	Sequence 179, App
482	96.4	482	27	US-60-327-731-8	Sequence 8, Appli
395	79.0	488	1	PCT-US02-29964-315	Sequence 315, App
395	79.0	488	27	US-60-327-731-10	Sequence 10, Appli
377	75.4	470	27	US-60-327-731-12	Sequence 12, Appli
342	68.4	502	1	PCT-US02-16639-5	Sequence 5, Appli
342	68.4	502	25	US-10-156-487A-5	Sequence 5, Appli
271	54.2	431	1	PCT-US00-35260-36	Sequence 36, Appli
271	54.2	431	23	US-09-912-935-36	Sequence 36, Appli
271	54.2	431	25	US-10-168-365-36	Sequence 36, Appli
229	45.8	240	25	US-10-104-047-3712	Sequence 3712, App
224	44.8	528	27	US-60-242-679-1283	Sequence 1283, App
24	26.0	146	1	PCT-US01-16450A-2453	Sequence 2453, App
130	26.0	146	1	PCT-US01-16450A-2453	Sequence 2453, App
108	21.6	205	1	PCT-US01-01354-16462	Sequence 16462, App
108	21.6	205	21	US-09-764-905-16462	Sequence 16462, A
108	21.6	205	24	US-10-092-399-16462	Sequence 16462, A
93	18.6	138	21	US-09-758-472-5729	Sequence 5729, App
93	18.6	138	26	US-10-235-926-5729	Sequence 5729, App
93	18.6	180	21	US-09-758-439-1069	Sequence 1069, App
93	18.6	180	26	US-10-201-915-1069	Sequence 1069, App
68	13.6	108	13	US-08-943-863A-38	Sequence 38, Appli
68	13.6	108	13	US-08-943-863B-38	Sequence 38, Appli
68	13.6	108	17	US-09-398-829-30	Sequence 30, Appli
53	10.6	53	1	PCT-US01-00663-32853	Sequence 32853, A
53	10.6	53	22	US-09-864-761-43750	Sequence 43750, A
53	10.6	53	25	US-10-182-993-31848	Sequence 31848, A
53	10.6	53	26	US-10-203-134-32631	Sequence 32631, A
53	10.6	53	26	US-10-203-135-31805	Sequence 31805, A
53	10.6	53	26	US-10-203-136-32859	Sequence 32859, A
53	10.6	53	26	US-10-203-137-32853	Sequence 32853, A
53	10.6	53	26	US-10-203-139-31726	Sequence 31726, A
41	8.2	306	1	PCT-US01-08631-39678	Sequence 39678, A
35	7.0	500	1	PCT-US01-24031-192	Sequence 192, App
35	7.0	500	1	PCT-US01-24031-292	Sequence 297, App
35	7.0	500	1	PCT-US02-08253-192	Sequence 192, App
35	7.0	500	1	PCT-US02-08253-297	Sequence 297, App
35	7.0	500	1	PCT-US02-16639-6	Sequence 6, Appli
35	7.0	500	23	US-09-918-715-192	Sequence 192, App
35	7.0	500	23	US-09-918-715-297	Sequence 297, App
35	7.0	500	25	US-10-156-487A-6	Sequence 6, Appli
18	3.6	18	27	US-60-327-731-7	Sequence 7, Appli
17	3.4	17	27	US-60-327-731-13	Sequence 13, Appli
13	2.6	1230	1	PCT-US01-08631-50433	Sequence 50433, A
10	2.0	118	22	US-09-867-550-198	Sequence 198, App
10	2.0	158	21	US-09-758-460-803	Sequence 803, App
10	2.0	158	25	US-10-144-702-803	Sequence 803, App
10	2.0	182	21	US-09-758-472-7142	Sequence 7142, App
10	2.0	182	26	US-10-235-926-7142	Sequence 7142, App
60	2.0	392	1	PCT-US00-35260-23	Sequence 23, Appli
61	2.0	392	1	PCT-US00-35260-25	Sequence 25, Appli
63	2.0	392	21	US-09-764-325A-23	Sequence 23, Appli
64	2.0	392	21	US-09-764-325A-25	Sequence 25, Appli
65	2.0	392	23	US-09-912-935-23	Sequence 23, Appli
66	2.0	392	23	US-09-912-935-25	Sequence 25, Appli
67	2.0	392	25	US-10-168-365-23	Sequence 23, Appli
68	2.0	392	25	US-10-168-365-25	Sequence 25, Appli
69	2.0	425	1	PCT-US00-35260-35	Sequence 35, Appli
70	2.0	425	23	US-09-912-935-35	Sequence 35, Appli
71	2.0	425	25	US-10-168-365-35	Sequence 35, Appli
72	2.0	427	18	US-09-488-725A-5784	Sequence 5784, App
73	2.0	427	18	US-09-488-725A-5785	Sequence 5785, App
74	2.0	435	27	US-60-327-731-14	Sequence 14, Appli
75	2.0	449	23	PCT-US00-35260-34	Sequence 34, Appli
76	2.0	449	23	US-09-912-935-34	Sequence 34, Appli
77	2.0	449	25	US-10-168-365-34	Sequence 34, Appli
78	2.0	486	18	US-09-488-725A-2212	Sequence 2212, App
79	2.0	499	1	PCT-US00-35260-31	Sequence 31, Appli

372	10	2.0	529	25	US-10-192-006-472	Sequence 472, App	445	10	2.0	529	25	US-10-197-693-472	Sequence 472, App
373	10	2.0	529	25	US-10-192-008-472	Sequence 472, App	446	10	2.0	529	25	US-10-197-694-472	Sequence 472, App
374	10	2.0	529	25	US-10-192-009-472	Sequence 472, App	447	10	2.0	529	25	US-10-197-695-472	Sequence 472, App
375	10	2.0	529	25	US-10-192-010-472	Sequence 472, App	448	10	2.0	529	25	US-10-197-696-472	Sequence 472, App
376	10	2.0	529	25	US-10-192-012-472	Sequence 472, App	449	10	2.0	529	25	US-10-197-697-472	Sequence 472, App
377	10	2.0	529	25	US-10-192-014-472	Sequence 472, App	450	10	2.0	529	25	US-10-197-698-472	Sequence 472, App
378	10	2.0	529	25	US-10-192-015-472	Sequence 472, App	451	10	2.0	529	25	US-10-197-699-472	Sequence 472, App
379	10	2.0	529	25	US-10-194-360-472	Sequence 472, App	452	10	2.0	529	25	US-10-197-700-472	Sequence 472, App
380	10	2.0	529	25	US-10-194-361-472	Sequence 472, App	453	10	2.0	529	25	US-10-197-701-472	Sequence 472, App
381	10	2.0	529	25	US-10-194-362-472	Sequence 472, App	454	10	2.0	529	25	US-10-197-702-472	Sequence 472, App
382	10	2.0	529	25	US-10-194-363-472	Sequence 472, App	455	10	2.0	529	25	US-10-197-703-472	Sequence 472, App
383	10	2.0	529	25	US-10-194-364-472	Sequence 472, App	456	10	2.0	529	25	US-10-197-704-472	Sequence 472, App
384	10	2.0	529	25	US-10-194-365-472	Sequence 472, App	457	10	2.0	529	25	US-10-197-705-472	Sequence 472, App
385	10	2.0	529	25	US-10-194-394-472	Sequence 472, App	458	10	2.0	529	25	US-10-197-706-472	Sequence 472, App
386	10	2.0	529	25	US-10-194-395-472	Sequence 472, App	459	10	2.0	529	25	US-10-197-707-472	Sequence 472, App
387	10	2.0	529	25	US-10-194-423-472	Sequence 472, App	460	10	2.0	529	25	US-10-197-708-472	Sequence 472, App
388	10	2.0	529	25	US-10-194-424-472	Sequence 472, App	461	10	2.0	529	25	US-10-197-709-472	Sequence 472, App
389	10	2.0	529	25	US-10-194-425-472	Sequence 472, App	462	10	2.0	529	25	US-10-197-710-472	Sequence 472, App
390	10	2.0	529	25	US-10-194-456-472	Sequence 472, App	463	10	2.0	529	25	US-10-197-711-472	Sequence 472, App
391	10	2.0	529	25	US-10-194-457-472	Sequence 472, App	464	10	2.0	529	25	US-10-198-757-472	Sequence 472, App
392	10	2.0	529	25	US-10-194-458-472	Sequence 472, App	465	10	2.0	529	25	US-10-198-758-472	Sequence 472, App
393	10	2.0	529	25	US-10-194-459-472	Sequence 472, App	466	10	2.0	529	25	US-10-198-759-472	Sequence 472, App
394	10	2.0	529	25	US-10-194-460-472	Sequence 472, App	467	10	2.0	529	25	US-10-198-760-472	Sequence 472, App
395	10	2.0	529	25	US-10-194-461-472	Sequence 472, App	468	10	2.0	529	25	US-10-198-761-472	Sequence 472, App
396	10	2.0	529	25	US-10-194-462-472	Sequence 472, App	469	10	2.0	529	25	US-10-198-762-472	Sequence 472, App
397	10	2.0	529	25	US-10-194-463-472	Sequence 472, App	470	10	2.0	529	25	US-10-198-763-472	Sequence 472, App
398	10	2.0	529	25	US-10-194-484-472	Sequence 472, App	471	10	2.0	529	25	US-10-198-764-472	Sequence 472, App
399	10	2.0	529	25	US-10-194-485-472	Sequence 472, App	472	10	2.0	529	25	US-10-198-765-472	Sequence 472, App
400	10	2.0	529	25	US-10-194-487-472	Sequence 472, App	473	10	2.0	529	25	US-10-198-766-472	Sequence 472, App
401	10	2.0	529	25	US-10-194-488-472	Sequence 472, App	474	10	2.0	529	25	US-10-198-767-472	Sequence 472, App
402	10	2.0	529	25	US-10-195-883-472	Sequence 472, App	475	10	2.0	529	25	US-10-198-768-472	Sequence 472, App
403	10	2.0	529	25	US-10-195-884-472	Sequence 472, App	476	10	2.0	529	25	US-10-198-769-472	Sequence 472, App
404	10	2.0	529	25	US-10-195-885-472	Sequence 472, App	477	10	2.0	529	25	US-10-198-770-472	Sequence 472, App
405	10	2.0	529	25	US-10-195-886-472	Sequence 472, App	478	10	2.0	529	25	US-10-198-771-472	Sequence 472, App
406	10	2.0	529	25	US-10-195-887-472	Sequence 472, App	479	10	2.0	529	25	US-10-199-301-472	Sequence 472, App
407	10	2.0	529	25	US-10-195-888-472	Sequence 472, App	480	10	2.0	529	25	US-10-199-302-472	Sequence 472, App
408	10	2.0	529	25	US-10-195-889-472	Sequence 472, App	481	10	2.0	529	25	US-10-199-303-472	Sequence 472, App
409	10	2.0	529	25	US-10-195-890-472	Sequence 472, App	482	10	2.0	529	25	US-10-199-304-472	Sequence 472, App
410	10	2.0	529	25	US-10-195-891-472	Sequence 472, App	483	10	2.0	529	25	US-10-199-305-472	Sequence 472, App
411	10	2.0	529	25	US-10-195-892-472	Sequence 472, App	484	10	2.0	529	25	US-10-199-307-472	Sequence 472, App
412	10	2.0	529	25	US-10-195-893-472	Sequence 472, App	485	10	2.0	529	25	US-10-199-308-472	Sequence 472, App
413	10	2.0	529	25	US-10-195-894-472	Sequence 472, App	486	10	2.0	529	25	US-10-199-309-472	Sequence 472, App
414	10	2.0	529	25	US-10-195-895-472	Sequence 472, App	487	10	2.0	529	25	US-10-199-310-472	Sequence 472, App
415	10	2.0	529	25	US-10-195-896-472	Sequence 472, App	488	10	2.0	529	25	US-10-199-311-472	Sequence 472, App
416	10	2.0	529	25	US-10-195-897-472	Sequence 472, App	489	10	2.0	529	25	US-10-199-312-472	Sequence 472, App
417	10	2.0	529	25	US-10-195-898-472	Sequence 472, App	490	10	2.0	529	25	US-10-199-313-472	Sequence 472, App
418	10	2.0	529	25	US-10-195-899-472	Sequence 472, App	491	10	2.0	529	25	US-10-199-314-472	Sequence 472, App
419	10	2.0	529	25	US-10-195-899-472	Sequence 472, App	492	10	2.0	529	25	US-10-199-315-472	Sequence 472, App
420	10	2.0	529	25	US-10-195-900-472	Sequence 472, App	493	10	2.0	529	25	US-10-199-316-472	Sequence 472, App
421	10	2.0	529	25	US-10-195-901-472	Sequence 472, App	494	10	2.0	529	25	US-10-199-317-472	Sequence 472, App
422	10	2.0	529	25	US-10-195-902-472	Sequence 472, App	495	10	2.0	529	25	US-10-199-318-472	Sequence 472, App
423	10	2.0	529	25	US-10-196-743-472	Sequence 472, App	496	10	2.0	529	25	US-10-199-345-472	Sequence 472, App
424	10	2.0	529	25	US-10-196-744-472	Sequence 472, App	497	10	2.0	529	25	US-10-199-457-472	Sequence 472, App
425	10	2.0	529	25	US-10-196-745-472	Sequence 472, App	498	10	2.0	529	25	US-10-199-458-472	Sequence 472, App
426	10	2.0	529	25	US-10-196-746-472	Sequence 472, App	499	10	2.0	529	25	US-10-199-459-472	Sequence 472, App
427	10	2.0	529	25	US-10-196-747-472	Sequence 472, App	500	10	2.0	529	25	US-10-199-460-472	Sequence 472, App
428	10	2.0	529	25	US-10-196-748-472	Sequence 472, App	501	10	2.0	529	25	US-10-199-461-472	Sequence 472, App
429	10	2.0	529	25	US-10-196-749-472	Sequence 472, App	502	10	2.0	529	25	US-10-199-669-472	Sequence 472, App
430	10	2.0	529	25	US-10-196-750-472	Sequence 472, App	503	10	2.0	529	25	US-10-199-663-472	Sequence 472, App
431	10	2.0	529	25	US-10-196-751-472	Sequence 472, App	504	10	2.0	529	25	US-10-199-664-472	Sequence 472, App
432	10	2.0	529	25	US-10-196-752-472	Sequence 472, App	505	10	2.0	529	25	US-10-199-665-472	Sequence 472, App
433	10	2.0	529	25	US-10-196-753-472	Sequence 472, App	506	10	2.0	529	25	US-10-199-666-472	Sequence 472, App
434	10	2.0	529	25	US-10-196-754-472	Sequence 472, App	507	10	2.0	529	25	US-10-199-667-472	Sequence 472, App
435	10	2.0	529	25	US-10-196-755-472	Sequence 472, App	508	10	2.0	529	25	US-10-199-668-472	Sequence 472, App
436	10	2.0	529	25	US-10-196-756-472	Sequence 472, App	509	10	2.0	529	25	US-10-199-669-472	Sequence 472, App
437	10	2.0	529	25	US-10-196-757-472	Sequence 472, App	510	10	2.0	529	25	US-10-199-670-472	Sequence 472, App
438	10	2.0	529	25	US-10-196-758-472	Sequence 472, App	511	10	2.0	529	25	US-10-199-673-472	Sequence 472, App
439	10	2.0	529	25	US-10-196-759-472	Sequence 472, App	512	10	2.0	529	26	US-10-200-617-472	Sequence 472, App
440	10	2.0	529	25	US-10-196-760-472	Sequence 472, App	513	10	2.0	529	26	US-10-201-321-472	Sequence 472, App
441	10	2.0	529	25	US-10-196-761-472	Sequence 472, App	514	10	2.0	529	26	US-10-201-322-472	Sequence 472, App
442	10	2.0	529	25	US-10-196-762-472	Sequence 472, App	515	10	2.0	529	26	US-10-201-323-472	Sequence 472, App
443	10	2.0	529	25	US-10-197-691-472	Sequence 472, App	516	10	2.0	529	26	US-10-201-325-472	Sequence 472, App
444	10	2.0	529	25	US-10-197-692-472	Sequence 472, App	517	10	2.0	529	26	US-10-201-326-472	Sequence 472, App

518	10	2.0	529	26	US-10-201-327-472	Sequence 472, App	591	10	2.0	529	26	US-10-205-909-472	Sequence 472, App
519	10	2.0	529	26	US-10-201-328-472	Sequence 472, App	592	10	2.0	529	26	US-10-205-910-472	Sequence 472, App
520	10	2.0	529	26	US-10-201-329-472	Sequence 472, App	593	10	2.0	529	26	US-10-206-907-472	Sequence 472, App
521	10	2.0	529	26	US-10-201-329-472	Sequence 472, App	594	10	2.0	529	26	US-10-206-909-472	Sequence 472, App
522	10	2.0	529	26	US-10-201-527-472	Sequence 472, App	595	10	2.0	529	26	US-10-206-910-472	Sequence 472, App
523	10	2.0	529	26	US-10-201-528-472	Sequence 472, App	596	10	2.0	529	26	US-10-206-911-472	Sequence 472, App
524	10	2.0	529	26	US-10-201-529-472	Sequence 472, App	597	10	2.0	529	26	US-10-206-912-472	Sequence 472, App
525	10	2.0	529	26	US-10-201-530-472	Sequence 472, App	598	10	2.0	529	26	US-10-206-913-472	Sequence 472, App
526	10	2.0	529	26	US-10-201-532-472	Sequence 472, App	599	10	2.0	529	26	US-10-206-914-472	Sequence 472, App
527	10	2.0	529	26	US-10-201-533-472	Sequence 472, App	600	10	2.0	529	26	US-10-206-915-472	Sequence 472, App
528	10	2.0	529	26	US-10-201-534-472	Sequence 472, App	601	10	2.0	529	26	US-10-206-916-472	Sequence 472, App
529	10	2.0	529	26	US-10-201-535-472	Sequence 472, App	602	10	2.0	529	26	US-10-206-917-472	Sequence 472, App
530	10	2.0	529	26	US-10-201-769-472	Sequence 472, App	603	10	2.0	529	26	US-10-206-918-472	Sequence 472, App
531	10	2.0	529	26	US-10-201-770-472	Sequence 472, App	604	10	2.0	529	26	US-10-206-919-472	Sequence 472, App
532	10	2.0	529	26	US-10-201-771-472	Sequence 472, App	605	10	2.0	529	26	US-10-206-920-472	Sequence 472, App
533	10	2.0	529	26	US-10-201-772-472	Sequence 472, App	606	10	2.0	529	26	US-10-206-921-472	Sequence 472, App
534	10	2.0	529	26	US-10-201-853-472	Sequence 472, App	607	10	2.0	529	26	US-10-206-922-472	Sequence 472, App
535	10	2.0	529	26	US-10-201-854-472	Sequence 472, App	608	10	2.0	529	26	US-10-206-923-472	Sequence 472, App
536	10	2.0	529	26	US-10-201-855-472	Sequence 472, App	609	10	2.0	529	26	US-10-206-924-472	Sequence 472, App
537	10	2.0	529	26	US-10-201-856-472	Sequence 472, App	610	10	2.0	529	26	US-10-206-925-472	Sequence 472, App
538	10	2.0	529	26	US-10-201-857-472	Sequence 472, App	611	10	2.0	529	26	US-10-206-926-472	Sequence 472, App
539	10	2.0	529	26	US-10-201-858-472	Sequence 472, App	612	10	2.0	529	26	US-10-206-927-472	Sequence 472, App
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543	10	2.0	529	26	US-10-202-411-472	Sequence 472, App	616	10	2.0	529	26	US-10-207-916-472	Sequence 472, App
544	10	2.0	529	26	US-10-202-412-472	Sequence 472, App	617	10	2.0	529	26	US-10-207-917-472	Sequence 472, App
545	10	2.0	529	26	US-10-202-413-472	Sequence 472, App	618	10	2.0	529	26	US-10-207-918-472	Sequence 472, App
546	10	2.0	529	26	US-10-202-469-472	Sequence 472, App	619	10	2.0	529	26	US-10-207-919-472	Sequence 472, App
547	10	2.0	529	26	US-10-202-470-472	Sequence 472, App	620	10	2.0	529	26	US-10-207-920-472	Sequence 472, App
548	10	2.0	529	26	US-10-202-471-472	Sequence 472, App	621	10	2.0	529	26	US-10-207-921-472	Sequence 472, App
549	10	2.0	529	26	US-10-202-472-472	Sequence 472, App	622	10	2.0	529	26	US-10-207-922-472	Sequence 472, App
550	10	2.0	529	26	US-10-202-473-472	Sequence 472, App	623	10	2.0	529	26	US-10-207-923-472	Sequence 472, App
551	10	2.0	529	26	US-10-202-474-472	Sequence 472, App	624	10	2.0	529	26	US-10-207-924-472	Sequence 472, App
552	10	2.0	529	26	US-10-202-475-472	Sequence 472, App	625	10	2.0	529	26	US-10-207-925-472	Sequence 472, App
553	10	2.0	529	26	US-10-202-476-472	Sequence 472, App	626	10	2.0	529	26	US-10-208-021-472	Sequence 472, App
554	10	2.0	529	26	US-10-202-934-472	Sequence 472, App	627	10	2.0	529	26	US-10-208-022-472	Sequence 472, App
555	10	2.0	529	26	US-10-202-935-472	Sequence 472, App	628	10	2.0	529	26	US-10-208-023-472	Sequence 472, App
556	10	2.0	529	26	US-10-202-936-472	Sequence 472, App	629	10	2.0	529	26	US-10-208-024-472	Sequence 472, App
557	10	2.0	529	26	US-10-202-937-472	Sequence 472, App	630	10	2.0	529	26	US-10-208-025-472	Sequence 472, App
558	10	2.0	529	26	US-10-202-938-472	Sequence 472, App	631	10	2.0	529	26	US-10-208-026-472	Sequence 472, App
559	10	2.0	529	26	US-10-202-939-472	Sequence 472, App	632	10	2.0	529	26	US-10-208-027-472	Sequence 472, App
560	10	2.0	529	26	US-10-202-940-472	Sequence 472, App	633	10	2.0	529	26	US-10-208-028-472	Sequence 472, App
561	10	2.0	529	26	US-10-202-941-472	Sequence 472, App	634	10	2.0	529	26	US-10-208-029-472	Sequence 472, App
562	10	2.0	529	26	US-10-202-942-472	Sequence 472, App	635	10	2.0	529	26	US-10-208-030-472	Sequence 472, App
563	10	2.0	529	26	US-10-205-502-472	Sequence 472, App	636	10	2.0	529	26	US-10-226-739-128	Sequence 128, App
564	10	2.0	529	26	US-10-205-503-472	Sequence 472, App	637	10	2.0	529	26	US-10-232-232-472	Sequence 472, App
565	10	2.0	529	26	US-10-205-504-472	Sequence 472, App	638	10	2.0	530	1	PCT-US01-24031-193	Sequence 193, App
566	10	2.0	529	26	US-10-205-505-472	Sequence 472, App	639	10	2.0	530	1	PCT-US01-24031-299	Sequence 299, App
567	10	2.0	529	26	US-10-205-506-472	Sequence 472, App	640	10	2.0	530	1	PCT-US02-08253-193	Sequence 193, App
568	10	2.0	529	26	US-10-205-507-472	Sequence 472, App	641	10	2.0	530	1	PCT-US02-08253-299	Sequence 299, App
569	10	2.0	529	26	US-10-205-508-472	Sequence 472, App	642	10	2.0	530	1	PCT-US02-16639-2	Sequence 2, Appl1
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571	10	2.0	529	26	US-10-205-510-472	Sequence 472, App	644	10	2.0	530	23	US-09-918-715-193	Sequence 193, App
572	10	2.0	529	26	US-10-205-511-472	Sequence 472, App	645	10	2.0	530	23	US-09-918-715-299	Sequence 299, App
573	10	2.0	529	26	US-10-205-512-472	Sequence 472, App	646	10	2.0	530	25	US-10-156-487A-2	Sequence 2, Appl1
574	10	2.0	529	26	US-10-205-890-472	Sequence 472, App	647	9	1.8	456	26	US-10-259-165-132	Sequence 132, App
575	10	2.0	529	26	US-10-205-891-472	Sequence 472, App	648	9	1.8	719	27	US-60-242-679-1423	Sequence 1423, App
576	10	2.0	529	26	US-10-205-893-472	Sequence 472, App	649	8	1.6	105	27	US-60-192-739-2382	Sequence 2382, App
577	10	2.0	529	26	US-10-205-894-472	Sequence 472, App	650	8	1.6	105	27	US-60-194-243-1705	Sequence 1705, App
578	10	2.0	529	26	US-10-205-895-472	Sequence 472, App	651	8	1.6	143	21	US-09-758-472-9461	Sequence 9461, App
579	10	2.0	529	26	US-10-205-896-472	Sequence 472, App	652	8	1.6	143	26	US-10-235-926-9461	Sequence 9461, App
580	10	2.0	529	26	US-10-205-897-472	Sequence 472, App	653	8	1.6	169	26	US-10-238-075-639	Sequence 639, App
581	10	2.0	529	26	US-10-205-898-472	Sequence 472, App	654	8	1.6	182	16	US-09-248-796-14937	Sequence 14937, A
582	10	2.0	529	26	US-10-205-899-472	Sequence 472, App	655	8	1.6	182	27	US-60-096-409-14937	Sequence 14937, A
583	10	2.0	529	26	US-10-205-900-472	Sequence 472, App	656	8	1.6	201	24	US-10-029-386-32993	Sequence 32993, A
584	10	2.0	529	26	US-10-205-901-472	Sequence 472, App	657	8	1.6	301	25	US-10-179-131-9453	Sequence 9453, A
585	10	2.0	529	26	US-10-205-902-472	Sequence 472, App	658	8	1.6	306	23	US-09-902-540-9859	Sequence 9859, App
586	10	2.0	529	26	US-10-205-903-472	Sequence 472, App	659	8	1.6	317	21	US-09-791-537-52224	Sequence 52224, A
587	10	2.0	529	26	US-10-205-904-472	Sequence 472, App	660	8	1.6	388	21	US-09-708-427-65103	Sequence 65103, A
588	10	2.0	529	26	US-10-205-905-472	Sequence 472, App	661	8	1.6	406	19	US-09-540-209B-8503	Sequence 8503, App
589	10	2.0	529	26	US-10-205-906-472	Sequence 472, App	662	8	1.6	417	21	US-09-708-427-65102	Sequence 65102, A
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665	8	1.6	625	27	US-60-167-217-3749	Sequence 3749, Ap	738	1.4	115	26	US-10-216-583-961	Sequence 961, App
666	8	1.6	625	27	US-60-191-637-3702	Sequence 3702, Ap	739	1.4	115	26	US-10-235-926-9117	Sequence 9117, Ap
667	8	1.6	889	22	US-09-829-472A-11	Sequence 11, Appl	740	1.4	115	27	US-60-195-053-2552	Sequence 2552, Ap
668	8	1.6	889	27	US-60-389-987-1925	Sequence 1925, Ap	741	1.4	120	20	US-09-617-682A-11158	Sequence 11158, A
669	8	1.6	889	27	US-60-412-418-1925	Sequence 1925, Ap	742	1.4	120	20	US-09-646-078-29	Sequence 29, Appl
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672	8	1.6	924	25	US-10-177-293-244	Sequence 244, App	745	1.4	121	21	US-09-708-427-84927	Sequence 84927, A
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676	8	1.6	1260	27	US-60-245-228-314	Sequence 314, App	749	1.4	122	21	US-09-708-427-84927	Sequence 84927, A
677	8	1.6	1266	25	US-10-177-488-154	Sequence 154, App	750	1.4	122	21	US-09-708-427-84927	Sequence 84927, A
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679	7	1.4	20	1	PCT-US96-19004A-23	Sequence 23, Appl	752	1.4	122	21	US-09-708-427-84927	Sequence 84927, A
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689	7	1.4	72	25	US-10-178-213-425	Sequence 425, App	762	1.4	122	21	US-09-708-427-84927	Sequence 84927, A
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722	7	1.4	109	18	PCT-US01-01431-70	Sequence 70, Appl	795	1.4	122	21	US-09-708-427-84927	Sequence 84927, A
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811	7	1.4	209	21	US-09-791-537-76208	Sequence 76208, A	884	7	1.4	332	19	US-09-513-996A-2728	Sequence 2728, Ap
812	7	1.4	209	23	US-09-995-493-128	Sequence 128, App	885	7	1.4	333	19	US-09-595-329A-1055	Sequence 1055, Ap
813	7	1.4	210	14	US-09-077-439A-25	Sequence 25, Appl	886	7	1.4	334	19	US-09-513-996A-2727	Sequence 2727, Ap
814	7	1.4	212	14	US-09-077-439A-26	Sequence 26, Appl	887	7	1.4	335	19	US-09-595-329A-1054	Sequence 1054, Ap
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818	7	1.4	217	20	US-09-614-150-27999	Sequence 27999, A	891	7	1.4	338	25	US-10-155-881-21818	Sequence 21818, A
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842	7	1.4	255	27	US-60-322-511-488	Sequence 488, App	915	7	1.4	388	1	PCT-US02-03987-11623	Sequence 11623, A
843	7	1.4	260	1	PCT-US99-22853B-154	Sequence 154, App	916	7	1.4	388	1	PCT-US98-06371-350	Sequence 350, App
844	7	1.4	260	20	US-09-614-150-16806	Sequence 16806, A	917	7	1.4	388	12	US-08-833-457-350	Sequence 350, App
845	7	1.4	260	20	US-09-688-051-84	Sequence 84, Appl	918	7	1.4	388	13	US-08-993-002A-5797	Sequence 5797, App
846	7	1.4	260	27	US-60-167-217-16837	Sequence 16837, A	919	7	1.4	388	22	US-09-815-242-11458	Sequence 11458, A
847	7	1.4	260	27	US-60-173-464-13793	Sequence 13793, A	920	7	1.4	388	22	US-09-815-242-11623	Sequence 11623, A
848	7	1.4	260	27	US-60-191-637-16850	Sequence 16850, A	921	7	1.4	388	22	US-09-881-752A-350	Sequence 350, App
849	7	1.4	260	27	US-60-191-681-13331	Sequence 13331, A	922	7	1.4	388	24	US-10-072-851-11458	Sequence 11458, A
850	7	1.4	264	27	US-60-243-468-1059	Sequence 1059, Ap	923	7	1.4	388	24	US-10-072-851-11623	Sequence 11623, A
851	7	1.4	267	1	PCT-US01-08631-33597	Sequence 33597, A	924	7	1.4	389	18	US-09-417-507-25430	Sequence 8738, A
852	7	1.4	270	21	US-09-738-626-5968	Sequence 5968, Ap	925	7	1.4	394	21	US-09-791-537-89738	Sequence 15525, A
853	7	1.4	274	1	PCT-US00-26524B-5039	Sequence 5039, Ap	926	7	1.4	395	27	US-60-360-039-15525	Sequence 15525, A
854	7	1.4	274	25	US-10-106-698-5049	Sequence 5049, Ap	927	7	1.4	395	27	US-60-360-039-16272	Sequence 16272, A
855	7	1.4	274	16	US-09-252-991A-19583	Sequence 19583, A	928	7	1.4	399	18	US-09-417-507-24386	Sequence 24386, A
856	7	1.4	291	16	US-09-270-767-33107	Sequence 33107, A	929	7	1.4	401	11	US-08-728-747-4	Sequence 4, Appl
857	7	1.4	291	16	US-09-270-767-48324	Sequence 48324, A	930	7	1.4	401	20	US-09-629-469A-17446	Sequence 17446, A
858	7	1.4	291	16	US-09-270-767-48324	Sequence 48324, A	931	7	1.4	401	27	US-60-389-987-1048	Sequence 1048, Ap
859	7	1.4	293	1	PCT-US01-08656-7556	Sequence 7556, Ap	932	7	1.4	401	27	US-60-412-418-1048	Sequence 1048, Ap
860	7	1.4	293	1	PCT-US01-01332-1150	Sequence 1150, Ap	933	7	1.4	403	27	US-60-360-039-15896	Sequence 15896, A
861	7	1.4	299	1	PCT-US01-01348-388	Sequence 388, App	934	7	1.4	403	27	US-09-252-691-8600	Sequence 8600, Ap
862	7	1.4	299	21	US-09-764-870-388	Sequence 388, App	935	7	1.4	405	16	US-09-252-691C-8600	Sequence 8600, Ap
863	7	1.4	299	21	US-09-764-870-388	Sequence 388, App	936	7	1.4	405	16	US-09-252-691C-8600	Sequence 8600, Ap
864	7	1.4	299	21	US-09-764-870-388	Sequence 388, App	937	7	1.4	406	21	US-09-791-537-97770	Sequence 97770, A
865	7	1.4	299	25	US-10-125-540-388	Sequence 388, App	938	7	1.4	406	21	US-10-219-999-48120	Sequence 48120, A
866	7	1.4	303	17	US-09-303-518D-690	Sequence 690, App	939	7	1.4	407	26	US-60-324-109-30117	Sequence 30117, A
867	7	1.4	304	24	US-10-015-127-13054	Sequence 13054, A	940	7	1.4	407	27	US-60-324-109-30117	Sequence 30117, A
868	7	1.4	310	21	US-09-791-537-30560	Sequence 30560, A	941	7	1.4	409	1	PCT-US02-07215-33	Sequence 33, Appl
869	7	1.4	313	1	PCT-US00-05881-741	Sequence 741, App	942	7	1.4	409	24	US-10-094-944-33	Sequence 33, Appl
870	7	1.4	313	23	US-09-925-298-741	Sequence 741, App	943	7	1.4	411	27	US-60-212-664-590	Sequence 590, App
871	7	1.4	313	25	US-10-102-806-741	Sequence 741, App	944	7	1.4	411	15	US-09-134-000-6481	Sequence 6481, Ap
872	7	1.4	316	19	US-09-543-681A-4590	Sequence 4590, Ap	945	7	1.4	416	21	US-09-708-427-51140	Sequence 51140, A
873	7	1.4	319	18	US-09-417-507-40259	Sequence 40259, A	946	7	1.4	416	21	US-09-708-427-51140	Sequence 51140, A
874	7	1.4	326	1	PCT-US02-07355-76	Sequence 76, Appl	947	7	1.4	417	17	US-09-254-472-7	Sequence 6, Appl
875	7	1.4	326	1	PCT-US02-07355-76	Sequence 76, Appl	948	7	1.4	417	17	US-09-382-088A-6	Sequence 6, Appl
876	7	1.4	330	15	US-09-154-707A-203	Sequence 203, App	949	7	1.4	417	21	US-09-708-427-69871	Sequence 69871, A
877	7	1.4	330	15	US-09-154-707A-203	Sequence 203, App	950	7	1.4	417	21	US-09-791-537-11207	Sequence 11207, A
878	7	1.4	330	16	US-09-270-767-44544	Sequence 44544, A	951	7	1.4	417	21	US-09-791-537-75456	Sequence 75456, A
879	7	1.4	330	23	US-09-966-262-203	Sequence 203, App	952	7	1.4	417	21	US-09-791-537-85854	Sequence 85854, A
880	7	1.4	330	23	US-09-983-966-203	Sequence 203, App	953	7	1.4	417	21	US-09-791-537-129593	Sequence 129593, A
881	7	1.4	330	23	US-09-984-245-203	Sequence 203, App	954	7	1.4	417	21	US-09-791-537-132269	Sequence 132269, A
882	7	1.4	330	24	US-10-059-395-203	Sequence 203, App	955	7	1.4	417	23	US-09-933-642-7	Sequence 7, Appl

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956 7 1.4 418 21 US-09-791-537-81081
957 7 1.4 419 1 PCT-US00-05988-1506
958 7 1.4 419 23 US-09-925-300-1506
959 7 1.4 421 21 US-09-758-472-9174
960 7 1.4 421 26 US-10-235-926-9174
961 7 1.4 423 20 US-09-605-703B-322
962 7 1.4 423 20 US-09-605-703B-324
963 7 1.4 423 21 US-09-738-626-3570
964 7 1.4 425 16 US-09-252-991A-31834
965 7 1.4 430 21 US-09-791-537-52328
966 7 1.4 432 23 US-09-925-388-8
967 7 1.4 433 21 US-09-791-537-32390
968 7 1.4 438 19 US-09-543-681A-9247
969 7 1.4 441 16 US-09-252-991A-24012
970 7 1.4 441 16 US-09-708-427-15243
971 7 1.4 443 22 US-09-855-768-900
972 7 1.4 449 1 PCT-US01-18569-2617
973 7 1.4 449 21 US-09-708-427-69870
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975 7 1.4 449 26 US-10-264-049-2617
976 7 1.4 452 21 US-09-791-537-36334
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978 7 1.4 453 21 US-09-708-427-14143
979 7 1.4 454 20 US-09-614-150-6111
980 7 1.4 454 27 US-60-167-217-6229
981 7 1.4 454 27 US-60-173-464-4391
982 7 1.4 454 27 US-60-191-637-6129
983 7 1.4 454 27 US-60-191-681-4803
984 7 1.4 458 26 US-10-219-999-39097
985 7 1.4 458 27 US-60-312-544-8622
986 7 1.4 458 21 US-09-791-537-110219
987 7 1.4 463 1 PCT-US02-07355-74
988 7 1.4 463 1 PCT-US02-18354-10
989 7 1.4 463 19 US-09-573-655A-716
990 7 1.4 463 19 US-09-573-655B-716
991 7 1.4 463 20 US-09-629-469A-14290
992 7 1.4 463 27 US-60-214-601-4
993 7 1.4 467 1 PCT-US02-07355-80
994 7 1.4 469 27 US-60-150-584-1022
995 7 1.4 469 27 US-60-360-039-5491
996 7 1.4 470 1 PCT-US01-18569-2916
997 7 1.4 470 21 US-09-791-537-126519
998 7 1.4 470 26 US-10-264-049-2916
999 7 1.4 471 6 US-08-203-905A-2
1000 7 1.4 471 21 US-09-791-537-121995
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ALIGNMENTS

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RESULT 1
PCT-US01-24031-230
; Sequence 230, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
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Sequence 81081, A
Sequence 1506, Ap
Sequence 1506, Ap
Sequence 9174, Ap
Sequence 9174, Ap
Sequence 322, App
Sequence 324, App
Sequence 3570, Ap
Sequence 31834, A
Sequence 52328, A
Sequence 8, Appli
Sequence 32390, A
Sequence 8247, Ap
Sequence 24012, A
Sequence 19243, A
Sequence 900, App
Sequence 2617, Ap
Sequence 69870, A
Sequence 22, Appli
Sequence 2617, Ap
Sequence 36334, A
Sequence 37844, A
Sequence 14143, A
Sequence 6111, Ap
Sequence 6229, Ap
Sequence 4991, Ap
Sequence 6129, Ap
Sequence 4803, Ap
Sequence 39097, A
Sequence 8622, Ap
Sequence 110219
Sequence 74, Appli
Sequence 10, Appli
Sequence 716, App
Sequence 716, App
Sequence 14290, A
Sequence 4, Appli
Sequence 80, Appli
Sequence 1022, Ap
Sequence 5491, Ap
Sequence 2916, Ap
Sequence 126519,
Sequence 2916, Ap
Sequence 2, Appli
Sequence 121995,
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PCT-US01-24031-230
Query Match 100.0%; Score 500; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGTGVGWNRRARESPGHVSEPD 60
Db 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGTGVGWNRRARESPGHVSEPD 60
QY 61 TQISQDLGGTTLAMDTLPNRTVRVVDNHNHYSYVSLYGPSEPHSRELWVDAEANSQVK 120
Db 61 TQISQDLGGTTLAMDTLPNRTVRVVDNHNHYSYVSLYGPSEPHSRELWVDAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSFDPFYGHPRLQITATGGTFMGDVTHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVVLSFDPFYGHPRLQITATGGTFMGDVTHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTTFVVOVDHVVYLOGWEDKSGFTFOAALHHDGRIVFAYKEI 240
Db 181 NFNPYSDNSTVYVFDNGTTFVVOVDHVVYLOGWEDKSGFTFOAALHHDGRIVFAYKEI 240
QY 241 SVPELSSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMGAVEPT 300
Db 241 SVPELSSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMGAVEPT 300
QY 301 LPTCLQHRSCDACMSDLTFNCSWCHVLQRCSSGDFDRYQEMMDYGCAGAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFNCSWCHVLQRCSSGDFDRYQEMMDYGCAGAEGRMCEDFQ 360
QY 361 DDHDSASPDTSFSDYDGLTSSSLFSDLSLTTDDDTKLNPYAGGDLQNNLSPKTKGT 420
Db 361 DDHDSASPDTSFSDYDGLTSSSLFSDLSLTTDDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLCTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLCTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQC 500
Db 481 YAEVPSGHEKEGFMFAEQC 500

RESULT 2
PCT-US02-08253-230
; Sequence 230, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-230
Query Match 100.0%; Score 500; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGTGVGWNRRARESPGHVSEPD 60
Db 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGTGVGWNRRARESPGHVSEPD 60
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Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSEPD 60
Qy 61 TQLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRRLWVDVAEANSQVK 120
Db 61 TQLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRRLWVDVAEANSQVK 120
Qy 121 IHTILSNTHQASRVLSFDPFPGHPLRQITITATGTFPMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHQASRVLSFDPFPGHPLRQITITATGTFPMGDVIRHMLTATQYVAPLMA 180
Qy 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRRSIFEHRIELDPKSVTSMAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRRSIFEHRIELDPKSVTSMAVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Qy 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTETDOKLNPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTETDOKLNPYAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

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RESULT 3

PCT-US02-29964-314
Sequence 314, Application PC/TUS0229964

GENERAL INFORMATION:

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; APPLICANT: Tang, X. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Duanrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03

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; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: dt_FL_genes Version 6.0
; SEQ ID NO 314
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-314

Query Match      100.0%; Score 500; DB 1; Length 500;
Best local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSEPD 60
Qy 61 TQLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRRLWVDVAEANSQVK 120
Db 61 TQLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRRLWVDVAEANSQVK 120
Qy 121 IHTILSNTHQASRVLSFDPFPGHPLRQITITATGTFPMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHQASRVLSFDPFPGHPLRQITITATGTFPMGDVIRHMLTATQYVAPLMA 180
Qy 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRRSIFEHRIELDPKSVTSMAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESRRRSIFEHRIELDPKSVTSMAVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Qy 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTETDOKLNPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTETDOKLNPYAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

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RESULT 4

US-09-918-715-230

Sequence 230, Application US/09918715

GENERAL INFORMATION:

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; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11

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; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230

Query Match      100.0%; Score 500; DB 23; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSDFDPFYGHPRLQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
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QY 121 IHTILSNTHROASRVVLSDFDPFYGHPRLQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFRYRQEMMDYGCQAEGRMCEDEFQ 360
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFRYRQEMMDYGCQAEGRMCEDEFQ 360
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 361 DEHDHSDASPDTSFSPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60

RESULT 5
US-60-327-731-5
; Sequence 5, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
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US-60-327-731-5

Query Match      100.0%; Score 500; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSDFDPFYGHPRLQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSDFDPFYGHPRLQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFRYRQEMMDYGCQAEGRMCEDEFQ 360
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFRYRQEMMDYGCQAEGRMCEDEFQ 360
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 361 DEHDHSDASPDTSFSPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60

RESULT 6
US-60-327-731-15
; Sequence 15, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-15

Query Match      100.0%; Score 500; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
QY 61 TOLSDQLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
DB 61 TOLSDQLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNGYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNGYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMIILNPSPDPVPESSRRRSIFFYHRIELDPKSVTMSAVEFT 300
DB 241 SVPEISSQHPVKTGLSDAFMIILNPSPDPVPESSRRRSIFFYHRIELDPKSVTMSAVEFT 300
QY 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
DB 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVEPSGHEKEGFMEEAEOC 500
DB 481 YAEVEPSGHEKEGFMEEAEOC 500

RESULT 7
PCT-US02-29964-804
; Sequence 804, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
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; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL-genes Version 6.0
; SEQ ID NO 804
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-804

Query Match 100.0%; Score 500; DB 1; Length 527;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 500; Conservative 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
DB 28 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 87
QY 61 TOLSDQLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
DB 88 TOLSDQLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 147
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 207
QY 181 NFNGYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 208 NFNGYSDNSTVYFDNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 267
QY 241 SVPEISSQHPVKTGLSDAFMIILNPSPDPVPESSRRRSIFFYHRIELDPKSVTMSAVEFT 300
DB 268 SVPEISSQHPVKTGLSDAFMIILNPSPDPVPESSRRRSIFFYHRIELDPKSVTMSAVEFT 327
QY 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
DB 328 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 387
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
DB 388 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGDGLQNNLSPKTKGT 447
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
DB 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
QY 481 YAEVEPSGHEKEGFMEEAEOC 500
DB 508 YAEVEPSGHEKEGFMEEAEOC 527

RESULT 8
PCT-US02-29964-805
; Sequence 805, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
```

APPLICANT: Goodrich, Ryle W.
APPLICANT: Weng, Gezhi
APPLICANT: Haley-Vicente, Dana
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 809ACIP PCT
CURRENT APPLICATION NUMBER: PCT/US02/29964
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,739
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 992
SOFTWARE: pt_FL_genes Version 6.0
SEQ ID NO 805
LENGTH: 527
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29964-805

Query Match 100.0%; Score 500; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 60
DB 28 MRGELWLLVLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 87
QY 61 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 120
DB 88 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 147
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 207
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 240
DB 208 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 267
QY 241 SVPEISSQHPVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 300
DB 268 SVPEISSQHPVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 327
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
DB 328 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 387
QY 361 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKTGT 420
DB 388 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKTGT 447
QY 421 PVHLGTIVGIVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 448 PVHLGTIVGIVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 507

QY 481 YAEVPSGHEKEGFMEEQC 500
DB 508 YAEVPSGHEKEGFMEEQC 527

RESULT 9

US-60-327-731-3
Sequence 3, Application US/60327731
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Ren, Feiyan
TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
FILE REFERENCE: HYS-44
CURRENT APPLICATION NUMBER: US/60/327,731
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 527
TYPE: PRT
ORGANISM: homo sapiens
US-60-327-731-3

Query Match 100.0%; Score 500; DB 27; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 60
DB 28 MRGELWLLVLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRARESPGHVSEPD 87
QY 61 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 120
DB 88 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 147
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 207
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 240
DB 208 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 267
QY 241 SVPEISSQHPVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 300
DB 268 SVPEISSQHPVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 327
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
DB 328 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 387
QY 361 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKTGT 420
DB 388 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKTGT 447
QY 421 PVHLGTIVGIVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 448 PVHLGTIVGIVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 507
QY 481 YAEVPSGHEKEGFMEEQC 500
DB 508 YAEVPSGHEKEGFMEEQC 527

RESULT 10
PCT-US01-24031-179
; Sequence 179, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-24031-179

Query Match 100.0%; Score 500; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 60
DB 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 562

QY 61 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPFSEPHSRELWVDVAEANRSQVK 120
DB 563 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPFSEPHSRELWVDVAEANRSQVK 622

QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 682

QY 181 NFNPGYSDNSTVVFNDGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVVFNDGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742

QY 241 SVPEISSQHPVKTGSLDAFMIPLNPSDPVPESSRRSIFEYHRIELDSPKVTSMASVEFTP 300
DB 743 SVPEISSQHPVKTGSLDAFMIPLNPSDPVPESSRRSIFEYHRIELDSPKVTSMASVEFTP 802

QY 301 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 862

QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
DB 863 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 922

QY 421 PVHLGTIVGIVLAVLLVAAILIAGIYINGHPTSNAAALFFIERPHHPAMKFRSHPDHST 480
DB 923 PVHLGTIVGIVLAVLLVAAILIAGIYINGHPTSNAAALFFIERPHHPAMKFRSHPDHST 982

QY 481 YAEVPSGHEKEGFMEEAQC 500
DB 983 YAEVPSGHEKEGFMEEAQC 1002

RESULT 11
PCT-US02-08253-179
; Sequence 179, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert

; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-179

Query Match 100.0%; Score 500; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 60
DB 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 562

QY 61 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPFSEPHSRELWVDVAEANRSQVK 120
DB 563 TQLSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPFSEPHSRELWVDVAEANRSQVK 622

QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 682

QY 181 NFNPGYSDNSTVVFNDGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVVFNDGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742

QY 241 SVPEISSQHPVKTGSLDAFMIPLNPSDPVPESSRRSIFEYHRIELDSPKVTSMASVEFTP 300
DB 743 SVPEISSQHPVKTGSLDAFMIPLNPSDPVPESSRRSIFEYHRIELDSPKVTSMASVEFTP 802

QY 301 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 862

QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
DB 863 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 922

QY 421 PVHLGTIVGIVLAVLLVAAILIAGIYINGHPTSNAAALFFIERPHHPAMKFRSHPDHST 480
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DB 983 YAEVPSGHEKEGFMEEAQC 1002

RESULT 12
US-09-918-715-179
; Sequence 179, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179

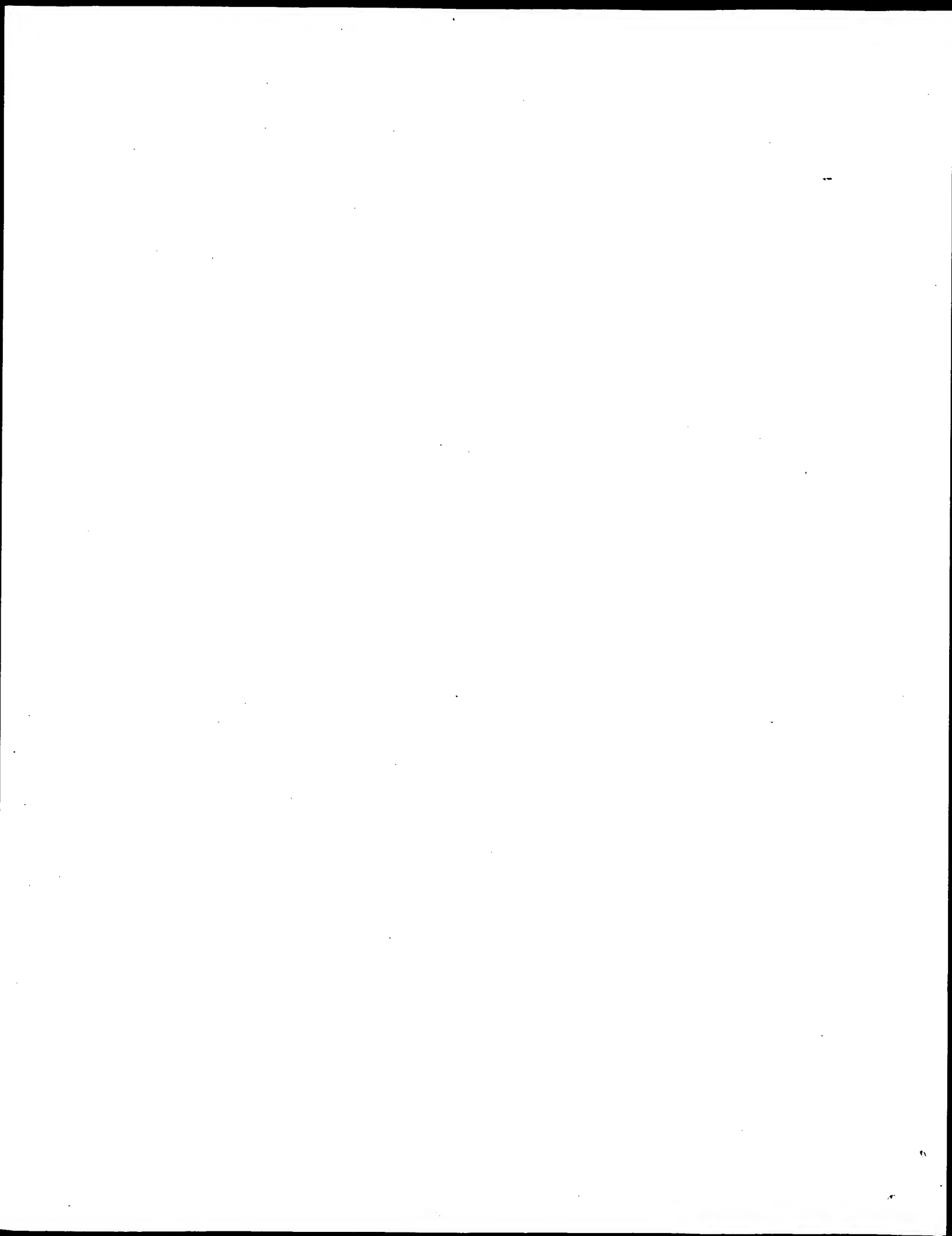
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QY 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
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DB 683 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742
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DB 803 LPTCLOHRSQASRVVLSDFPFYGHPLRQITITATGGFIFMGDVIHRLMTATQYVAPLMA 360
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QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
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QY 481 YAEVPSGHEKEGPMWAEQC 500
DB 983 YAEVPSGHEKEGPMWAEQC 1002

RESULT 13
PCT-US02-29964-731-8
; Sequence 8, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482

; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-8

Query Match 96.4%; Score 482; DB 27; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 79 DNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 138
DB 61 DNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 120
QY 139 FDPFPGHPLRQITITATGGFIFMGDVIHRLMTATQYVAPLMAFNPNGYSDNSTVYFDNG 198
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QY 199 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 258
DB 181 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 240
QY 259 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTPCTCLOHRSQASRVVLS 318
DB 241 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTPCTCLOHRSQASRVVLS 300
QY 319 TFNCSCWCHVLQRCSSGFDRIYQWMDYGCQAEGRMCEDFODEHDSASPTSPYDG 378
DB 301 TFNCSCWCHVLQRCSSGFDRIYQWMDYGCQAEGRMCEDFODEHDSASPTSPYDG 360
QY 379 DLTTSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPTKGTTPVHLGTIVGIVLAVLLVA 438
DB 361 DLTTSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPTKGTTPVHLGTIVGIVLAVLLVA 420
QY 439 AILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGPMWAE 498
DB 421 AILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGPMWAE 480
QY 499 QC 500
DB 481 QC 482

RESULT 14
PCT-US02-29964-315
; Sequence 315, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Ailong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Ghosh, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radjic T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 809ACIP ECT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21



GenCore version 5.1.4_p5_4578
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Run on: April 22, 2003, 16:17:11 ; Search time 79 Seconds
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Title: US-09-918-715-230

Perfect score: 500

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	500	100.0	527	6	US-10-266-252-3
6	482	96.4	482	6	US-10-266-252-8
7	427	85.4	427	7	US-60-453-135-13630
8	427	85.4	427	7	US-60-453-050-13630
9	395	79.0	488	6	US-10-266-252-10
10	377	75.4	470	6	US-10-266-252-12
11	371	74.2	400	6	US-10-218-140-5790
12	130	26.0	146	6	US-10-264-237-2453
13	18	3.6	18	6	US-10-266-252-7
14	17	3.4	17	6	US-10-266-252-13
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16	10	2.0	379	7	US-60-452-680-20245
17	10	2.0	435	6	US-10-266-252-14
18	10	2.0	529	6	US-10-125-923A-472
19	10	2.0	529	6	US-10-205-892-472
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21	10	2.0	529	6	US-10-174-575A-472
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23	10	2.0	529	6	US-10-187-749-472
24	10	2.0	529	6	US-10-199-672-472
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29	8	1.6	505	6	US-10-156-761-14310	Sequence 14310, A
30	8	1.6	924	1	PCT-US02-19669A-244	Sequence 244, App
31	8	1.6	1004	1	PCT-US02-07283-58	Sequence 58, Appl
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34	7	1.4	8	5	US-09-641-528-14793	Sequence 14793, A
35	7	1.4	8	5	US-09-641-528-14900	Sequence 14900, A
36	7	1.4	8	5	US-09-641-528-28138	Sequence 28138, A
37	7	1.4	8	5	US-09-641-528-45901	Sequence 45901, A
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83	7	1.4	11	5	US-09-641-528-14887	Sequence 14887, A
84	7	1.4	11	5	US-09-641-528-14890	Sequence 14890, A
85	7	1.4	11	5	US-09-641-528-22746	Sequence 22746, A
86	7	1.4	11	5	US-09-641-528-22750	Sequence 22750, A
87	7	1.4	11	5	US-09-641-528-28141	Sequence 28141, A
88	7	1.4	11	5	US-09-641-528-45904	Sequence 45904, A
89	7	1.4	11	5	US-09-641-528-45927	Sequence 45927, A
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93	7	1.4	11	5	US-09-641-528A-14796	Sequence 14796, A
94	7	1.4	11	5	US-09-641-528A-14887	Sequence 14887, A
95	7	1.4	11	5	US-09-641-528A-14890	Sequence 14890, A
96	7	1.4	11	5	US-09-641-528A-22746	Sequence 22746, A
97	7	1.4	11	5	US-09-641-528A-22750	Sequence 22750, A
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99	7	1.4	11	5	US-09-641-528A-45904	Sequence 45904, A

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102	7	1.4	7	15	5	US-09-641-528A-47633	Sequence 47633, A	175	7	1.4	340	6	US-10-366-683-29871	Sequence 29871, A
103	7	1.4	7	15	5	US-09-641-528A-47648	Sequence 47648, A	176	7	1.4	346	6	US-10-366-683-14945	Sequence 14945, A
104	7	1.4	7	15	5	US-09-641-528A-47650	Sequence 47650, A	177	7	1.4	348	6	US-10-369-493-19684	Sequence 19684, A
105	7	1.4	7	15	5	US-09-641-528A-47651	Sequence 47651, A	178	7	1.4	377	6	US-10-366-683-24649	Sequence 24649, A
106	7	1.4	7	15	5	US-09-641-528A-47621	Sequence 47621, A	179	7	1.4	388	6	US-10-282-122A-59031	Sequence 59031, A
107	7	1.4	7	15	5	US-09-641-528A-47633	Sequence 47633, A	180	7	1.4	388	6	US-10-335-977-5797	Sequence 5797, A
108	7	1.4	7	15	5	US-09-641-528A-47648	Sequence 47648, A	181	7	1.4	395	6	US-10-369-493-15525	Sequence 15525, A
109	7	1.4	7	15	5	US-09-641-528A-47650	Sequence 47650, A	182	7	1.4	403	5	US-10-369-493-16891	Sequence 16891, A
110	7	1.4	7	15	5	US-09-641-528A-47651	Sequence 47651, A	183	7	1.4	403	5	US-09-949-016-8892	Sequence 8892, A
111	7	1.4	7	68	1	PCT-US02-32727-6277	Sequence 6277, A	184	7	1.4	403	5	US-10-369-493-15896	Sequence 15896, A
112	7	1.4	7	68	6	US-09-978-825-6277	Sequence 6277, A	185	7	1.4	411	7	US-60-453-135-9757	Sequence 9757, A
113	7	1.4	7	68	6	US-10-149-136-57	Sequence 57, Appl	186	7	1.4	411	7	US-60-453-135-9758	Sequence 9758, A
114	7	1.4	7	75	6	US-10-188-246-24	Sequence 24, Appl	187	7	1.4	411	7	US-60-453-050-9758	Sequence 9758, A
115	7	1.4	7	97	6	US-10-188-246-24	Sequence 24, Appl	188	7	1.4	411	7	US-60-453-050-9758	Sequence 9758, A
116	7	1.4	7	97	6	US-10-188-246-24	Sequence 24, Appl	189	7	1.4	411	7	US-60-453-050-9758	Sequence 9758, A
117	7	1.4	7	99	6	PCT-US02-21360-22	Sequence 21, Appl	190	7	1.4	411	7	US-60-453-050-9758	Sequence 9758, A
118	7	1.4	7	101	6	US-10-188-246-22	Sequence 22, Appl	191	7	1.4	413	5	US-09-134-000C-6481	Sequence 6481, A
119	7	1.4	7	101	6	US-10-188-246-22	Sequence 22, Appl	192	7	1.4	413	5	US-09-134-000C-6481	Sequence 6481, A
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121	7	1.4	7	112	6	US-10-277-802-70	Sequence 70, Appl	194	7	1.4	415	6	US-10-405-027-3704	Sequence 3704, A
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123	7	1.4	7	114	1	PCT-US02-32727-25797	Sequence 25797, A	196	7	1.4	417	5	US-09-949-016-6482	Sequence 6482, A
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130	7	1.4	7	129	5	US-09-978-825-7531	Sequence 7531, A	203	7	1.4	422	6	US-09-949-016-9518	Sequence 9518, A
131	7	1.4	7	129	5	US-10-057-498-7531	Sequence 7531, A	204	7	1.4	425	6	US-10-366-683-31834	Sequence 31834, A
132	7	1.4	7	137	5	US-09-675-784A-7983	Sequence 7983, A	205	7	1.4	439	7	US-60-443-566-4365	Sequence 4365, A
133	7	1.4	7	144	6	US-10-282-122A-49872	Sequence 49872, A	206	7	1.4	439	7	US-60-453-444-8375	Sequence 8375, A
134	7	1.4	7	144	6	US-10-156-761-10524	Sequence 10524, A	207	7	1.4	441	6	US-10-366-683-24012	Sequence 24012, A
135	7	1.4	7	191	5	US-09-675-784A-8693	Sequence 8693, A	208	7	1.4	449	5	US-09-769-736-135	Sequence 135, A
136	7	1.4	7	194	5	US-09-828-455-27	Sequence 27, Appl	209	7	1.4	449	5	US-09-949-016-9515	Sequence 9515, A
137	7	1.4	7	197	6	US-09-828-455-29	Sequence 29, Appl	210	7	1.4	449	5	US-09-949-016-9516	Sequence 9516, A
138	7	1.4	7	204	5	US-09-949-002-457	Sequence 457, Appl	211	7	1.4	463	6	US-10-094-886A-74	Sequence 74, Appl
139	7	1.4	7	204	5	US-09-949-002-457	Sequence 457, Appl	212	7	1.4	463	6	US-10-312-354-8	Sequence 8, Appl
140	7	1.4	7	213	6	US-10-156-761-9250	Sequence 9250, A	213	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
141	7	1.4	7	215	6	US-10-156-761-9250	Sequence 9250, A	214	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
142	7	1.4	7	221	6	PCT-US02-35136-9	Sequence 9, Appl	215	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
143	7	1.4	7	227	6	US-10-366-683-25207	Sequence 25207, A	216	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
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145	7	1.4	7	229	5	US-09-978-825-18027	Sequence 18027, A	218	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
146	7	1.4	7	229	5	US-10-057-498-18027	Sequence 18027, A	219	7	1.4	463	6	US-10-094-886A-80	Sequence 80, Appl
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161	7	1.4	7	282	5	US-09-978-825-23151	Sequence 23151, A	234	7	1.4	529	7	US-60-452-680-12463	Sequence 12463, A
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163	7	1.4	7	315	5	US-09-724-676A-78602	Sequence 78602, A	236	7	1.4	545	6	US-10-369-493-7880	Sequence 7880, A
164	7	1.4	7	315	5	US-09-724-676A-78605	Sequence 78605, A	237	7	1.4	554	6	US-10-366-683-23813	Sequence 23813, A
165	7	1.4	7	315	5	US-09-724-676A-78605	Sequence 78605, A	238	7	1.4	561	6	US-10-282-122A-72403	Sequence 72403, A
166	7	1.4	7	321	6	US-10-282-122A-66162	Sequence 66162, A	239	7	1.4	596	6	US-10-369-493-1211	Sequence 1211, A
167	7	1.4	7	326	6	US-10-094-886-76	Sequence 76, Appl	240	7	1.4	608	6	US-10-366-683-22327	Sequence 22327, A
168	7	1.4	7	326	6	US-10-094-886-76	Sequence 76, Appl	241	7	1.4	611	6	US-10-366-683-20097	Sequence 20097, A
169	7	1.4	7	326	6	US-10-094-886A-76	Sequence 76, Appl	242	7	1.4	613	6	US-10-369-493-18239	Sequence 18239, A
170	7	1.4	7	326	6	US-10-094-886A-76	Sequence 76, Appl	243	7	1.4	623	5	US-09-724-676A-54584	Sequence 54584, A
171	7	1.4	7	327	6	US-10-282-122A-64027	Sequence 64027, A	244	7	1.4	631	5	PCT-US02-37777-38	Sequence 38, Appl
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247	7	1.4	643	6	US-10-282-122A-77602	Sequence 77602, A	320	7	1.4	1184	6	US-10-127-844A-412	Sequence 412, App
248	7	1.4	654	6	US-10-366-683-31667	Sequence 31667, A	321	7	1.4	1184	6	US-10-127-845A-412	Sequence 412, App
249	7	1.4	660	5	US-09-724-676-78601	Sequence 78601, A	322	7	1.4	1184	6	US-10-127-846A-412	Sequence 412, App
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252	7	1.4	660	5	US-09-724-676A-78604	Sequence 78604, A	325	7	1.4	1184	6	US-10-127-851A-412	Sequence 412, App
253	7	1.4	660	6	US-10-263-929-110	Sequence 110, App	326	7	1.4	1184	6	US-10-127-852A-412	Sequence 412, App
254	7	1.4	664	6	US-10-156-761-12753	Sequence 12753, App	327	7	1.4	1184	6	US-10-127-900A-412	Sequence 412, App
255	7	1.4	675	6	US-10-366-683-23185	Sequence 23185, A	328	7	1.4	1184	6	US-10-128-687A-412	Sequence 412, App
256	7	1.4	686	7	US-60-452-680-22413	Sequence 22413, A	329	7	1.4	1184	6	US-10-128-688A-412	Sequence 412, App
257	7	1.4	686	7	US-60-452-680-22413	Sequence 22413, A	330	7	1.4	1184	6	US-10-128-692A-412	Sequence 412, App
258	7	1.4	686	7	US-60-453-135-13882	Sequence 13882, A	331	7	1.4	1184	6	US-10-128-694A-412	Sequence 412, App
259	7	1.4	701	6	US-60-446-775-338	Sequence 338, App	332	7	1.4	1184	6	US-10-131-816A-412	Sequence 412, App
260	7	1.4	709	6	US-10-161-493-76	Sequence 76, Appl	333	7	1.4	1184	6	US-10-131-817A-412	Sequence 412, App
261	7	1.4	713	6	US-10-156-761-11362	Sequence 11362, A	334	7	1.4	1184	6	US-10-131-818A-412	Sequence 412, App
262	7	1.4	767	6	US-10-366-683-28262	Sequence 28262, A	335	7	1.4	1184	6	US-10-131-820A-412	Sequence 412, App
263	7	1.4	794	1	PCT-US02-28859-76	Sequence 76, Appl	336	7	1.4	1184	6	US-10-131-835A-412	Sequence 412, App
264	7	1.4	794	6	US-10-241-220-76	Sequence 76, Appl	337	7	1.4	1184	6	US-10-127-826A-412	Sequence 412, App
265	7	1.4	885	6	US-10-282-122A-43753	Sequence 43753, A	338	7	1.4	1184	6	US-10-127-828A-412	Sequence 412, App
266	7	1.4	1019	6	US-10-094-749-2609	Sequence 2609, App	339	7	1.4	1184	6	US-10-127-833A-412	Sequence 412, App
267	7	1.4	1065	6	US-10-282-122A-64932	Sequence 64932, A	340	7	1.4	1184	6	US-10-131-825A-412	Sequence 412, App
268	7	1.4	1093	6	US-10-369-493-10885	Sequence 10885, A	341	7	1.4	1184	6	US-10-137-869A-412	Sequence 412, App
269	7	1.4	1120	6	US-10-369-493-1495	Sequence 1495, App	342	7	1.4	1184	6	US-10-128-691A-412	Sequence 412, App
270	7	1.4	1144	7	US-60-452-680-22415	Sequence 22415, A	343	7	1.4	1184	6	US-10-131-815A-412	Sequence 412, App
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272	7	1.4	1144	7	US-60-453-050-13884	Sequence 13884, A	345	7	1.4	1184	6	US-10-131-822A-412	Sequence 412, App
273	7	1.4	1184	5	US-09-989-733-124	Sequence 124, App	346	7	1.4	1184	6	US-10-131-828A-412	Sequence 412, App
274	7	1.4	1184	5	US-09-992-643-124	Sequence 124, App	347	7	1.4	1184	6	US-10-158-787-412	Sequence 412, App
275	7	1.4	1184	6	US-10-131-813A-412	Sequence 412, App	348	7	1.4	1184	6	US-10-147-488-412	Sequence 412, App
276	7	1.4	1184	6	US-10-131-819A-412	Sequence 412, App	349	7	1.4	1245	7	US-60-453-135-7844	Sequence 7844, App
277	7	1.4	1184	6	US-10-131-823A-412	Sequence 412, App	350	7	1.4	1245	7	US-60-453-135-7845	Sequence 7845, App
278	7	1.4	1184	6	US-10-131-824A-412	Sequence 412, App	351	7	1.4	1245	7	US-60-453-050-7844	Sequence 7844, App
279	7	1.4	1184	6	US-10-131-826A-412	Sequence 412, App	352	7	1.4	1245	7	US-60-453-050-7845	Sequence 7845, App
280	7	1.4	1184	6	US-10-131-829A-412	Sequence 412, App	353	7	1.4	1250	7	US-60-449-155-64	Sequence 64, Appl
281	7	1.4	1184	6	US-10-125-926A-412	Sequence 412, App	354	7	1.4	1269	6	US-10-282-122A-62237	Sequence 62237, A
282	7	1.4	1184	6	US-10-127-829A-412	Sequence 412, App	355	7	1.4	1308	7	US-60-453-135-7843	Sequence 7843, App
283	7	1.4	1184	6	US-10-127-831A-412	Sequence 412, App	356	7	1.4	1308	7	US-60-453-050-7843	Sequence 7843, App
284	7	1.4	1184	6	US-10-127-835A-412	Sequence 412, App	357	7	1.4	1308	7	US-60-452-680-22414	Sequence 22414, A
285	7	1.4	1184	6	US-10-127-837A-412	Sequence 412, App	358	7	1.4	1330	7	US-60-453-135-13883	Sequence 13883, A
286	7	1.4	1184	6	US-10-127-842A-412	Sequence 412, App	359	7	1.4	1330	7	US-60-453-050-13883	Sequence 13883, A
287	7	1.4	1184	6	US-10-127-850A-412	Sequence 412, App	360	6	1.2	7	6	US-10-293-580-31	Sequence 31, Appl
288	7	1.4	1184	6	US-10-127-901A-412	Sequence 412, App	361	6	1.2	8	5	US-09-641-528-6037	Sequence 6037, App
289	7	1.4	1184	6	US-10-128-689A-412	Sequence 412, App	362	6	1.2	8	5	US-09-641-528-6588	Sequence 6588, App
290	7	1.4	1184	6	US-10-131-830A-412	Sequence 412, App	363	6	1.2	8	5	US-09-641-528-6624	Sequence 6624, App
291	7	1.4	1184	6	US-10-131-833A-412	Sequence 412, App	364	6	1.2	8	5	US-09-641-528-14449	Sequence 14449, A
292	7	1.4	1184	6	US-10-131-837A-412	Sequence 412, App	365	6	1.2	8	5	US-09-641-528-14859	Sequence 14859, A
293	7	1.4	1184	6	US-10-125-930A-412	Sequence 412, App	366	6	1.2	8	5	US-09-641-528-22452	Sequence 22452, A
294	7	1.4	1184	6	US-10-127-825A-412	Sequence 412, App	367	6	1.2	8	5	US-09-641-528-22747	Sequence 22747, A
295	7	1.4	1184	6	US-10-127-825A-412	Sequence 412, App	368	6	1.2	8	5	US-09-641-528-28094	Sequence 28094, A
296	7	1.4	1184	6	US-10-127-843A-412	Sequence 412, App	369	6	1.2	8	5	US-09-641-528A-6037	Sequence 6037, App
297	7	1.4	1184	6	US-10-127-849A-412	Sequence 412, App	370	6	1.2	8	5	US-09-641-528A-6588	Sequence 6588, App
298	7	1.4	1184	6	US-10-128-684A-412	Sequence 412, App	371	6	1.2	8	5	US-09-641-528A-6624	Sequence 6624, App
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302	7	1.4	1184	6	US-10-128-693A-412	Sequence 412, App	375	6	1.2	8	5	US-09-641-528A-22747	Sequence 22747, A
303	7	1.4	1184	6	US-10-131-821A-412	Sequence 412, App	376	6	1.2	8	5	US-09-641-528A-28094	Sequence 28094, A
304	7	1.4	1184	6	US-10-131-836A-412	Sequence 412, App	377	6	1.2	9	5	US-09-189-702A-117	Sequence 117, App
305	7	1.4	1184	6	US-10-137-872A-412	Sequence 412, App	378	6	1.2	9	5	US-09-641-528-1025	Sequence 1025, App
306	7	1.4	1184	6	US-10-137-873A-412	Sequence 412, App	379	6	1.2	9	5	US-09-641-528-1133	Sequence 1133, App
307	7	1.4	1184	6	US-10-125-921A-412	Sequence 412, App	380	6	1.2	9	5	US-09-641-528-6044	Sequence 6044, App
308	7	1.4	1184	6	US-10-125-928A-412	Sequence 412, App	381	6	1.2	9	5	US-09-641-528-14450	Sequence 14450, A
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316	7	1.4	1184	6	US-10-127-836A-412	Sequence 412, App	389	6	1.2	9	5	US-09-641-528A-1153	Sequence 1153, App
317	7	1.4	1184	6	US-10-127-839A-412	Sequence 412, App	390	6	1.2	9	5	US-09-641-528A-6044	Sequence 6044, App
318	7	1.4	1184	6	US-10-127-840A-412	Sequence 412, App	391	6	1.2	9	5	US-09-641-528A-14450	Sequence 14450, A

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394	6	1.2	9	5	US-09-641-528A-22455	Sequence 22455, A	467	6	1.2	52	6	US-10-057-498-14560	Sequence 14560, A
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396	6	1.2	9	5	US-09-641-528A-35848	Sequence 35848, A	469	6	1.2	53	1	PCT-US02-32727-2532	Sequence 2532, Ap
397	6	1.2	9	5	US-09-641-528A-35848	Sequence 35848, A	470	6	1.2	53	5	US-09-978-825-2532	Sequence 2532, Ap
398	6	1.2	10	5	US-09-189-702A-152	Sequence 152, App	471	6	1.2	53	5	US-09-864-408A-1036	Sequence 1036, Ap
399	6	1.2	10	5	US-09-189-702A-153	Sequence 153, App	472	6	1.2	53	5	US-09-864-408A-8076	Sequence 8076, Ap
400	6	1.2	10	5	US-09-641-528-6216	Sequence 6216, Ap	473	6	1.2	53	6	US-10-057-498-2532	Sequence 2532, Ap
401	6	1.2	10	5	US-09-641-528-6589	Sequence 6589, Ap	474	6	1.2	53	6	US-10-218-140-1142	Sequence 1142, Ap
402	6	1.2	10	5	US-09-641-528-6612	Sequence 6612, Ap	475	6	1.2	54	1	PCT-US02-32727-21407	Sequence 21407, A
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408	6	1.2	10	5	US-09-641-528A-22745	Sequence 22745, A	481	6	1.2	56	5	US-09-724-676-91592	Sequence 91592, A
409	6	1.2	10	5	US-09-641-528A-28096	Sequence 28096, A	482	6	1.2	56	5	US-09-724-676A-91592	Sequence 91592, A
410	6	1.2	10	5	US-09-641-528A-35774	Sequence 35774, A	483	6	1.2	56	6	US-10-282-122A-57361	Sequence 57361, A
411	6	1.2	11	5	US-09-641-528-1154	Sequence 1154, Ap	484	6	1.2	57	5	US-09-864-408A-6222	Sequence 6222, Ap
412	6	1.2	11	5	US-09-641-528-6038	Sequence 6038, Ap	485	6	1.2	58	6	US-10-315-023-15	Sequence 15, Appl
413	6	1.2	11	5	US-09-641-528-6103	Sequence 6103, Ap	486	6	1.2	59	1	PCT-US02-32727-19633	Sequence 19633, A
414	6	1.2	11	5	US-09-641-528-14451	Sequence 14451, A	487	6	1.2	59	5	US-09-978-825-19633	Sequence 19633, A
415	6	1.2	11	5	US-09-641-528-14861	Sequence 14861, A	488	6	1.2	59	6	US-10-057-498-19633	Sequence 19633, A
416	6	1.2	11	5	US-09-641-528-22454	Sequence 22454, A	489	6	1.2	59	6	US-10-243-475-93	Sequence 93, Appl
417	6	1.2	11	5	US-09-641-528-22572	Sequence 22572, A	490	6	1.2	60	1	PCT-US02-32727-3865	Sequence 3865, Ap
418	6	1.2	11	5	US-09-641-528-22572	Sequence 22572, A	491	6	1.2	60	5	US-09-513-999C-6713	Sequence 6713, Ap
419	6	1.2	11	5	US-09-641-528-22572	Sequence 22572, A	492	6	1.2	60	5	US-09-978-825-3865	Sequence 3865, Ap
420	6	1.2	11	5	US-09-641-528-22735	Sequence 22735, A	493	6	1.2	60	5	US-09-513-999C-6713	Sequence 6713, Ap
421	6	1.2	11	5	US-09-641-528-22735	Sequence 22735, A	494	6	1.2	60	6	US-10-057-498-3865	Sequence 3865, Ap
422	6	1.2	11	5	US-09-641-528-27725	Sequence 27725, A	495	6	1.2	61	1	PCT-US02-32727-9646	Sequence 9646, Ap
423	6	1.2	11	5	US-09-641-528-28097	Sequence 28097, A	496	6	1.2	61	5	US-10-203-138A-11887	Sequence 11887, A
424	6	1.2	11	5	US-09-641-528-36069	Sequence 36069, A	497	6	1.2	61	5	US-09-513-999C-6266	Sequence 6266, Ap
425	6	1.2	11	5	US-09-641-528-36407	Sequence 36407, A	498	6	1.2	61	5	US-09-978-825-9646	Sequence 9646, Ap
426	6	1.2	11	5	US-09-641-528A-1154	Sequence 1154, Ap	499	6	1.2	61	5	US-09-864-408A-7754	Sequence 7754, Ap
427	6	1.2	11	5	US-09-641-528A-6038	Sequence 6038, Ap	500	6	1.2	61	5	US-09-513-999C-6266	Sequence 6266, Ap
428	6	1.2	11	5	US-09-641-528A-6103	Sequence 6103, Ap	501	6	1.2	61	6	US-10-057-498-9646	Sequence 9646, Ap
429	6	1.2	11	5	US-09-641-528A-14451	Sequence 14451, A	502	6	1.2	62	1	PCT-US02-32727-1656	Sequence 1656, Ap
430	6	1.2	11	5	US-09-641-528A-14861	Sequence 14861, A	503	6	1.2	62	6	US-09-978-825-1656	Sequence 1656, Ap
431	6	1.2	11	5	US-09-641-528A-22454	Sequence 22454, A	504	6	1.2	62	6	US-10-057-498-1656	Sequence 1656, Ap
432	6	1.2	11	5	US-09-641-528A-22572	Sequence 22572, A	505	6	1.2	62	6	US-10-203-138A-12709	Sequence 12709, A
433	6	1.2	11	5	US-09-641-528A-27725	Sequence 27725, A	506	6	1.2	64	5	US-09-513-999C-6113	Sequence 6113, Ap
434	6	1.2	11	5	US-09-641-528A-28097	Sequence 28097, A	507	6	1.2	64	5	US-09-724-676A-65952	Sequence 65952, A
435	6	1.2	11	5	US-09-641-528A-36069	Sequence 36069, A	508	6	1.2	64	5	US-09-724-676A-65952	Sequence 65952, A
436	6	1.2	11	5	US-09-641-528A-36407	Sequence 36407, A	509	6	1.2	64	5	US-09-513-999C-6113	Sequence 6113, Ap
437	6	1.2	11	5	US-09-641-528A-50701	Sequence 50701, A	510	6	1.2	65	1	PCT-US02-32727-17827	Sequence 17827, A
438	6	1.2	15	5	US-09-641-528A-50701	Sequence 50701, A	511	6	1.2	65	5	US-09-978-825-17827	Sequence 17827, A
439	6	1.2	15	5	US-09-641-528A-50701	Sequence 50701, A	512	6	1.2	65	5	US-10-057-498-17827	Sequence 17827, A
440	6	1.2	19	6	US-10-030-850-14	Sequence 14, Appl	513	6	1.2	65	5	US-09-864-408A-8998	Sequence 8998, Ap
441	6	1.2	19	6	US-10-030-850-14	Sequence 14, Appl	514	6	1.2	66	5	US-09-864-408A-8998	Sequence 8998, Ap
442	6	1.2	20	1	PCT-US02-34021-358	Sequence 358, App	515	6	1.2	67	1	PCT-US02-32727-15283	Sequence 15283, A
443	6	1.2	20	6	US-10-225-567A-861	Sequence 861, App	516	6	1.2	67	5	PCT-US02-32727-20738	Sequence 20738, A
444	6	1.2	20	6	US-10-280-066-358	Sequence 358, App	517	6	1.2	67	5	US-09-978-825-15283	Sequence 15283, A
445	6	1.2	21	5	US-09-721-708A-107	Sequence 107, App	518	6	1.2	67	6	US-09-978-825-20738	Sequence 20738, A
446	6	1.2	21	5	US-09-721-708A-107	Sequence 107, App	519	6	1.2	67	6	US-10-057-498-15283	Sequence 15283, A
447	6	1.2	21	6	US-10-109-048-926	Sequence 926, App	520	6	1.2	67	6	US-10-057-498-20738	Sequence 20738, A
448	6	1.2	29	6	US-10-306-631-81	Sequence 81, App	521	6	1.2	68	5	US-09-513-999C-7136	Sequence 7136, Ap
449	6	1.2	35	6	US-10-341-200-18	Sequence 18, Appl	522	6	1.2	69	1	PCT-US02-32727-13796	Sequence 13796, Ap
450	6	1.2	40	6	US-10-031-167-11	Sequence 11, Appl	523	6	1.2	69	5	US-09-978-825-13796	Sequence 13796, A
451	6	1.2	44	6	US-10-203-138A-10667	Sequence 10667, A	524	6	1.2	69	6	US-10-057-498-13796	Sequence 13796, A
452	6	1.2	47	1	PCT-US02-40655-382	Sequence 382, App	525	6	1.2	72	1	PCT-US02-32727-12935	Sequence 12935, A
453	6	1.2	48	6	US-10-282-122A-44263	Sequence 44263, A	526	6	1.2	72	1	PCT-US02-32727-13629	Sequence 13629, A
454	6	1.2	50	1	PCT-US02-32727-23637	Sequence 23637, A	527	6	1.2	72	1	PCT-US02-32727-27291	Sequence 27291, A
455	6	1.2	50	5	US-09-978-825-23637	Sequence 23637, A	528	6	1.2	72	5	US-09-978-825-12935	Sequence 12935, A
456	6	1.2	50	6	US-10-057-498-23637	Sequence 23637, A	529	6	1.2	72	5	US-09-978-825-13629	Sequence 13629, A
457	6	1.2	51	1	PCT-US02-32727-24818	Sequence 24818, A	530	6	1.2	72	5	US-09-978-825-27291	Sequence 27291, A
458	6	1.2	51	6	US-09-978-825-24818	Sequence 24818, A	531	6	1.2	72	6	US-10-057-498-12935	Sequence 12935, A
459	6	1.2	51	6	US-10-057-498-24818	Sequence 24818, A	532	6	1.2	72	6	US-10-057-498-13629	Sequence 13629, A
460	6	1.2	52	1	PCT-US02-32727-9460	Sequence 9460, Ap	533	6	1.2	72	6	US-10-057-498-27291	Sequence 27291, A
461	6	1.2	52	1	PCT-US02-32727-14560	Sequence 14560, A	534	6	1.2	73	1	PCT-US02-32727-23785	Sequence 23785, A
462	6	1.2	52	1	PCT-US02-32727-20815	Sequence 20815, A	535	6	1.2	73	1	PCT-US02-32727-26667	Sequence 26667, A
463	6	1.2	52	5	US-09-978-825-9460	Sequence 9460, Ap	536	6	1.2	73	1	PCT-US02-30050-64	Sequence 64, Appl
464	6	1.2	52	5	US-09-978-825-14560	Sequence 14560, A	537	6	1.2	73	5	US-09-978-825-23785	Sequence 23785, A

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539	6	1.2	73	6	US-10-057-498-23785	Sequence 23785, A	612	6	1.2	97	6	US-10-057-498-801	Sequence 801, App
540	6	1.2	73	6	US-10-057-498-26667	Sequence 26667, A	613	6	1.2	97	6	US-10-057-498-14364	Sequence 14364, A
541	6	1.2	73	6	US-10-252-945-75	Sequence 75, Appl	614	6	1.2	98	1	PCT-US02-36123-32	Sequence 32, Appl
542	6	1.2	73	6	US-10-156-761-11956	Sequence 11956, A	615	6	1.2	98	1	US-10-203-138A-12470	Sequence 12470, A
543	6	1.2	75	6	US-10-403-340-4	Sequence 4, Appl	616	6	1.2	99	6	US-10-282-122A-51632	Sequence 51632, A
544	6	1.2	75	7	US-60-452-680-15538	Sequence 15538, A	617	6	1.2	100	1	PCT-US02-32727-6106	Sequence 6106, App
545	6	1.2	75	7	US-60-452-680-15539	Sequence 15539, A	618	6	1.2	100	1	PCT-US03-04649-9	Sequence 9, Appl
546	6	1.2	76	1	PCT-US02-32727-848	Sequence 848, App	619	6	1.2	100	5	US-09-978-825-6106	Sequence 6106, App
547	6	1.2	76	1	PCT-US02-32727-30499	Sequence 30499, A	620	6	1.2	100	5	US-09-864-408A-7456	Sequence 7456, App
548	6	1.2	76	5	US-09-978-825-848	Sequence 848, App	621	6	1.2	100	5	US-10-057-498-6106	Sequence 6106, App
549	6	1.2	76	5	US-09-978-825-30499	Sequence 30499, A	622	6	1.2	100	7	US-60-438-000-91	Sequence 91, Appl
550	6	1.2	76	6	US-10-057-498-848	Sequence 848, App	623	6	1.2	100	7	US-60-455-444-6258	Sequence 6258, App
551	6	1.2	77	5	US-09-864-408A-5768	Sequence 5768, App	624	6	1.2	101	1	PCT-US02-32727-23884	Sequence 23884, App
552	6	1.2	77	6	US-10-209-582-900	Sequence 900, App	625	6	1.2	101	1	PCT-US02-32727-30715	Sequence 30715, A
553	6	1.2	77	6	US-10-403-340-5	Sequence 5, Appl	626	6	1.2	101	5	US-09-978-825-23884	Sequence 23884, A
554	6	1.2	78	1	PCT-US02-32727-29042	Sequence 29042, A	627	6	1.2	101	5	US-09-978-825-30715	Sequence 30715, A
555	6	1.2	78	5	US-09-978-825-29042	Sequence 29042, A	628	6	1.2	101	6	US-10-057-498-23884	Sequence 23884, A
556	6	1.2	78	6	US-10-057-498-29042	Sequence 29042, A	629	6	1.2	101	6	US-10-300-616-47	Sequence 47, Appl
557	6	1.2	80	1	PCT-US02-32727-1161	Sequence 1161, App	630	6	1.2	103	5	US-09-724-676-73652	Sequence 73652, A
558	6	1.2	80	1	PCT-US02-32727-2109	Sequence 2109, App	631	6	1.2	103	5	US-09-724-676-73653	Sequence 73653, A
559	6	1.2	80	5	US-09-978-825-1161	Sequence 1161, App	632	6	1.2	103	5	US-09-724-676-73654	Sequence 73654, A
560	6	1.2	80	5	US-09-978-825-2109	Sequence 2109, App	633	6	1.2	103	5	US-09-724-676A-73652	Sequence 73652, A
561	6	1.2	80	5	US-09-978-825-7115	Sequence 7115, App	634	6	1.2	103	5	US-09-724-676A-73653	Sequence 73653, A
562	6	1.2	80	5	US-09-978-825-7115	Sequence 7115, App	635	6	1.2	103	5	US-09-724-676A-73654	Sequence 73654, A
563	6	1.2	80	6	US-10-057-498-1161	Sequence 1161, App	636	6	1.2	104	1	PCT-US02-32727-15857	Sequence 15857, A
564	6	1.2	80	6	US-10-057-498-2109	Sequence 2109, App	637	6	1.2	104	1	PCT-US02-32727-29965	Sequence 29965, A
565	6	1.2	80	6	US-10-057-498-7115	Sequence 7115, App	638	6	1.2	104	5	US-09-724-676-79428	Sequence 79428, A
566	6	1.2	81	1	PCT-US02-32727-18424	Sequence 18424, A	639	6	1.2	104	5	US-09-724-676A-79428	Sequence 79428, A
567	6	1.2	81	5	US-09-978-825-18424	Sequence 18424, A	640	6	1.2	104	5	US-09-978-825-15857	Sequence 15857, A
568	6	1.2	81	6	US-10-057-498-18424	Sequence 18424, A	641	6	1.2	104	5	US-09-978-825-29965	Sequence 29965, A
569	6	1.2	81	6	US-10-351-334-325	Sequence 325, App	642	6	1.2	104	6	US-10-057-498-15857	Sequence 15857, A
570	6	1.2	82	5	US-09-513-999C-4382	Sequence 4382, App	643	6	1.2	105	5	US-09-864-408A-9050	Sequence 9050, App
571	6	1.2	82	5	US-09-513-999C-4382	Sequence 4382, App	644	6	1.2	105	5	PCT-US02-32727-25943	Sequence 25943, A
572	6	1.2	82	6	US-10-351-334-234	Sequence 234, App	645	6	1.2	106	5	US-09-978-825-25943	Sequence 25943, A
573	6	1.2	83	1	PCT-US02-32727-25149	Sequence 25149, A	646	6	1.2	106	6	US-10-057-498-25943	Sequence 25943, A
574	6	1.2	83	5	US-09-978-825-25149	Sequence 25149, A	647	6	1.2	107	1	PCT-US02-32727-822	Sequence 822, App
575	6	1.2	83	6	US-10-057-498-25149	Sequence 25149, A	648	6	1.2	107	5	US-09-978-825-822	Sequence 822, App
576	6	1.2	83	6	US-10-380-731-852	Sequence 852, App	649	6	1.2	107	6	US-10-057-498-822	Sequence 822, App
577	6	1.2	84	6	US-10-335-977-9188	Sequence 9188, App	650	6	1.2	109	1	PCT-US02-32727-11859	Sequence 11859, A
578	6	1.2	84	7	US-60-453-135-10280	Sequence 10280, A	651	6	1.2	109	1	PCT-US02-32727-14716	Sequence 14716, A
579	6	1.2	84	7	US-60-453-050-10280	Sequence 10280, A	652	6	1.2	109	5	US-09-978-825-11859	Sequence 11859, A
580	6	1.2	85	1	PCT-US02-32727-397	Sequence 397, App	653	6	1.2	109	5	US-09-978-825-14716	Sequence 14716, A
581	6	1.2	85	5	US-09-978-825-397	Sequence 397, App	654	6	1.2	109	6	US-10-057-498-11859	Sequence 11859, A
582	6	1.2	85	6	US-10-057-498-397	Sequence 397, App	655	6	1.2	109	6	US-10-057-498-14716	Sequence 14716, A
583	6	1.2	86	6	US-10-363-936-347	Sequence 347, App	656	6	1.2	109	6	US-10-203-138A-10619	Sequence 10619, A
584	6	1.2	88	1	PCT-US02-32727-17909	Sequence 17909, A	657	6	1.2	109	6	US-10-276-781-1377	Sequence 1377, App
585	6	1.2	88	1	PCT-US02-32727-19296	Sequence 19296, A	658	6	1.2	110	1	PCT-US02-32727-23018	Sequence 23018, A
586	6	1.2	88	5	US-09-950-084-7372	Sequence 7372, App	659	6	1.2	110	5	US-09-513-999C-7883	Sequence 7883, App
587	6	1.2	88	5	US-09-978-825-17909	Sequence 17909, A	660	6	1.2	110	5	US-09-978-825-23018	Sequence 23018, A
588	6	1.2	88	5	US-09-978-825-19296	Sequence 19296, A	661	6	1.2	110	5	US-09-513-999C-7883	Sequence 7883, App
589	6	1.2	88	6	US-10-057-498-17909	Sequence 17909, A	662	6	1.2	110	6	US-10-057-498-23018	Sequence 23018, A
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591	6	1.2	89	6	US-10-277-802-76	Sequence 76, Appl	664	6	1.2	111	6	US-10-335-977-9189	Sequence 9189, App
592	6	1.2	89	6	US-10-282-122A-65530	Sequence 65530, A	665	6	1.2	112	1	PCT-US02-32727-21993	Sequence 21993, A
593	6	1.2	89	6	US-10-282-122A-65598	Sequence 65598, A	666	6	1.2	112	5	US-09-978-825-21993	Sequence 21993, A
594	6	1.2	89	6	US-10-382-122A-76751	Sequence 76751, A	667	6	1.2	112	6	US-10-057-498-21993	Sequence 21993, A
595	6	1.2	92	6	US-10-094-886A-194	Sequence 194, App	668	6	1.2	112	6	US-10-156-761-12166	Sequence 12166, A
596	6	1.2	92	6	US-10-094-886A-194	Sequence 194, App	669	6	1.2	113	5	US-09-949-016-7586	Sequence 7586, App
597	6	1.2	95	1	PCT-US02-32727-3990	Sequence 3990, App	670	6	1.2	113	5	US-10-282-122A-57655	Sequence 57655, A
598	6	1.2	95	1	PCT-US02-32727-28407	Sequence 28407, A	671	6	1.2	114	5	US-09-724-676-86956	Sequence 86956, A
599	6	1.2	95	5	US-09-724-676-83238	Sequence 83238, A	672	6	1.2	114	5	US-09-724-676-86957	Sequence 86957, A
600	6	1.2	95	5	US-09-724-676A-83238	Sequence 83238, A	673	6	1.2	114	5	US-09-724-676A-86957	Sequence 86957, A
601	6	1.2	95	5	US-09-978-825-3990	Sequence 3990, App	674	6	1.2	114	5	PCT-US02-32727-30846	Sequence 30846, A
602	6	1.2	95	5	US-09-978-825-28407	Sequence 28407, A	675	6	1.2	115	5	US-09-978-825-30846	Sequence 30846, A
603	6	1.2	95	6	US-10-057-498-3990	Sequence 3990, App	676	6	1.2	115	5	US-09-864-408A-7730	Sequence 7730, App
604	6	1.2	95	6	US-10-057-498-28407	Sequence 28407, A	677	6	1.2	115	5	US-10-264-237-1496	Sequence 1496, App
605	6	1.2	96	6	US-10-333-610-13	Sequence 13, Appl	678	6	1.2	115	6	US-10-276-781-1129	Sequence 1129, App
606	6	1.2	97	1	PCT-US02-32727-801	Sequence 801, App	679	6	1.2	115	6	US-10-351-334-324	Sequence 324, App
607	6	1.2	97	1	PCT-US02-32727-14364	Sequence 14364, A	680	6	1.2	115	6	PCT-US02-32727-9004	Sequence 9004, App
608	6	1.2	97	1	PCT-US02-32727-29917	Sequence 29917, A	681	6	1.2	117	5	US-09-978-825-9004	Sequence 9004, App
609	6	1.2	97	5	US-09-978-825-801	Sequence 801, App	682	6	1.2	117	5	US-10-057-498-9004	Sequence 9004, App
610	6	1.2	97	5	US-09-978-825-14364	Sequence 14364, A	683	6	1.2	117	6	US-10-057-498-9004	Sequence 9004, App

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585	1.2	118	5	US-09-724-676A-59394	Sequence 59394, A	758	6	1.2	151	5	US-09-675-784A-9833	Sequence 9833, Ap
586	1.2	118	5	US-09-724-676A-59394	Sequence 59394, A	759	6	1.2	151	5	US-10-156-761-13736	Sequence 13736, A
587	1.2	118	5	US-09-978-825-12213	Sequence 12213, A	760	6	1.2	152	1	PCT-US02-32727-8473	Sequence 67, Appl
588	1.2	118	5	US-10-057-498-12213	Sequence 12213, A	761	6	1.2	153	1	PCT-US02-32727-8473	Sequence 8473, Ap
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978 6 1.2 226 6 US-10-199-672-122 Sequence 122, App
979 6 1.2 226 6 US-10-194-486-122 Sequence 122, App
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983 6 1.2 228 6 US-10-156-761-13668 Sequence 13668, A
984 6 1.2 230 1 PCT-US02-32727-13771 Sequence 13771, A
985 6 1.2 230 5 US-09-978-825-13771 Sequence 13771, A
986 6 1.2 230 6 US-10-057-498-13771 Sequence 13771, A
987 6 1.2 231 6 US-10-369-493-8364 Sequence 8364, App
988 6 1.2 232 5 US-09-724-676-64863 Sequence 64863, A
989 6 1.2 232 5 US-09-724-676-64863 Sequence 64863, A
990 6 1.2 233 1 PCT-US02-36123-3044 Sequence 3044, App
991 6 1.2 233 6 US-10-282-122A-74685 Sequence 74685, A
992 6 1.2 234 5 US-09-724-676-64898 Sequence 64898, A
993 6 1.2 234 5 US-09-724-676A-64898 Sequence 64898, A
994 6 1.2 234 6 US-10-366-683-17302 Sequence 17302, A
995 6 1.2 234 6 US-10-289-762-241 Sequence 241, App
996 6 1.2 236 6 US-10-276-774-2408 Sequence 2408, App
997 6 1.2 236 6 US-10-282-122A-57603 Sequence 57603, A
998 6 1.2 237 6 US-10-264-237-1929 Sequence 1929, App
999 6 1.2 238 6 US-10-282-122A-72127 Sequence 72127, A
1000 6 1.2 238 6 US-10-369-493-757 Sequence 757, App
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ALIGNMENTS

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RESULT 1
US-10-266-252-5
; Sequence 5, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-5
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Query Match 100.0%; Score 500; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
QY 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHRAQSRVLSDFPFYCHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRAQSRVLSDFPFYCHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
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QY 181 NFNPGYSDNSTVVFYDNGTGVVQNDHVYLOGWEDKSGTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVVFYDNGTGVVQNDHVYLOGWEDKSGTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTLGSLDAFMIINPSPDVPESRRRSIFEYHRIELDPKSVTSMSAVEFTP 300
DB 241 SVPEISSQHPVKTLGSLDAFMIINPSPDVPESRRRSIFEYHRIELDPKSVTSMSAVEFTP 300
QY 301 LPTCLOHRSKDCACMSDLTFNCSWCHVLRQSSGDFDRYQEWMDYGCQAQEAAGRMCEDFQ 360
DB 301 LPTCLOHRSKDCACMSDLTFNCSWCHVLRQSSGDFDRYQEWMDYGCQAQEAAGRMCEDFQ 360
QY 361 DEDHDSASDPTSFSPYDGLTDTSSSLFTDSTLTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
DB 361 DEDHDSASDPTSFSPYDGLTDTSSSLFTDSTLTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKGFMEAEQC 500
DB 481 YAEVPSGHEKGFMEAEQC 500
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RESULT 2

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US-10-266-252-15
; Sequence 15, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-15
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Query Match 100.0%; Score 500; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60
QY 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHRAQSRVLSDFPFYCHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRAQSRVLSDFPFYCHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVVFYDNGTGVVQNDHVYLOGWEDKSGTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVVFYDNGTGVVQNDHVYLOGWEDKSGTFOAALHHDGRIVFAYKEIPM 240
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QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEEAEOC 500
DB 481 YAEVPSGHEKEGFMEEAEOC 500

RESULT 3
US-60-453-135-13631
; Sequence 13631, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13631

Query Match 100.0%; Score 500; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
DB 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
DB 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
QY 121 IHTILSNTHRQASRVVLSDFDPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRQASRVVLSDFDPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEEAEOC 500
DB 481 YAEVPSGHEKEGFMEEAEOC 500

RESULT 4
US-60-453-050-13631
; Sequence 13631, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13631

Query Match 100.0%; Score 500; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
DB 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
DB 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
QY 121 IHTILSNTHRQASRVVLSDFDPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRQASRVVLSDFDPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEEAEOC 500
DB 481 YAEVPSGHEKEGFMEEAEOC 500

RESULT 5
US-10-266-252-3
; Sequence 3, Application US/10266252
; GENERAL INFORMATION:

; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Ren, Feiyan
 ; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
 ; FILE REFERENCE: HYS-44A
 ; CURRENT APPLICATION NUMBER: US/10/266,252
 ; PRIOR FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: 60/327,731
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 3:
 ; LENGTH: 527
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-266-252-3

Query Match 100.0%; Score 500; DB 6; Length 527;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
 DB 28 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 87
 QY 61 TQLSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 120
 DB 88 TQLSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 147
 QY 121 IHTILSNTHROASRVLSDFPPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMA 180
 DB 148 IHTILSNTHROASRVLSDFPPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMA 207
 QY 181 NFNPYSDNSTVYVFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 208 NFNPYSDNSTVYVFDNGTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPM 267
 QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTP 300
 DB 268 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTP 327
 QY 301 LPTCLOHRSQDACSMDLTFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQ 360
 DB 328 LPTCLOHRSQDACSMDLTFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQ 387
 QY 361 DEDHDSASPTSFSPYDGLDTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
 DB 388 DEDHDSASPTSFSPYDGLDTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 447
 QY 421 PVHLGTIVGLVAVLLVAAILLAGIYNGHPTSNAAFFIERRPHHPWPAKFRSHPDHST 480
 DB 448 PVHLGTIVGLVAVLLVAAILLAGIYNGHPTSNAAFFIERRPHHPWPAKFRSHPDHST 507
 QY 481 YAEVPSGHEKEGFMEEQC 500
 DB 508 YAEVPSGHEKEGFMEEQC 527

RESULT 6
 US-10-266-252-8
 ; Sequence 8, Application US/10266252
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Ren, Feiyan
 ; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
 ; FILE REFERENCE: HYS-44A
 ; CURRENT APPLICATION NUMBER: US/10/266,252
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: 60/327,731
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-266-252-8

Query Match 96.4%; Score 482; DB 6; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 LSPQPCAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 78
 DB 1 LSPQPCAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 60
 QY 79 DNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVLS 138
 DB 61 DNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVLS 120
 QY 139 FDFPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMAFNPNPGYSDNSTVYVFDNG 198
 DB 121 FDFPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMAFNPNPGYSDNSTVYVFDNG 180
 QY 199 TVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSD 258
 DB 181 TVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSD 240
 QY 259 AFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTPCTCLOHRSQDACSMDL 318
 DB 241 AFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTPCTCLOHRSQDACSMDL 300
 QY 319 TFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQDEHDSASPTSFSPYD 378
 DB 301 TFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQDEHDSASPTSFSPYD 360
 QY 379 DLTTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGLVAVLLVA 438
 DB 361 DLTTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGLVAVLLVA 420
 QY 439 AILLAGIYNGHPTSNAAFFIERRPHHPWPAKFRSHPDHSTYAEVPSGHEKEGFMEE 498
 DB 421 AILLAGIYNGHPTSNAAFFIERRPHHPWPAKFRSHPDHSTYAEVPSGHEKEGFMEE 480
 QY 499 QC 500
 DB 481 QC 482

RESULT 7
 US-60-453-135-13630
 ; Sequence 13630, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001456
 ; CURRENT APPLICATION NUMBER: US/60/453,135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762

Db 181 NPNPGYSDNSTVVFVDFDNGTFFVQWMDHVVYLOGWEDKSGFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTP 300
Db 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLLTE 395
Db 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLLTE 395
RESULT 10
US-10-266-252-12
; Sequence 12, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 470
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-12

Query Match 75.4%; Score 377; DB 6; Length 470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 LSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTLP 78
Db 1 LSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTLP 60
QY 79 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKTHTILSNTHROASRVLS 138
Db 61 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKTHTILSNTHROASRVLS 120
QY 139 FDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMAFNPNPGYSDNSTVVFVDFDNG 198
Db 121 FDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMAFNPNPGYSDNSTVVFVDFDNG 180
QY 199 TVFVQWHDVYLOGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPISSSQHPVKTKGLSD 258
Db 181 TVFVQWHDVYLOGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPISSSQHPVKTKGLSD 240
QY 259 AFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 318
Db 241 AFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 300
QY 319 TFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQEDHDSASPDTSFSPYDG 378
Db 301 TFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQEDHDSASPDTSFSPYDG 360
QY 379 DLTTSSSLFIDSLLTE 395
| | | | |

Db 361 DLTTSSSLFIDSLLTE 377
RESULT 11
US-10-218-140-5790
; Sequence 5790, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5790
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: "Xaa" = "Any Amino Acid"
US-10-218-140-5790

Query Match 74.2%; Score 371; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPD 60
Db 29 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPD 88
QY 61 TOLSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQV 120
Db 89 TOLSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQV 148
QY 121 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 180
Db 149 IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 208
QY 181 NPNPGYSDNSTVVFVDFDNGTFFVQWMDHVVYLOGWEDKSGFTFOAALHHDGRIVFAYKEIPM 240
Db 209 NPNPGYSDNSTVVFVDFDNGTFFVQWMDHVVYLOGWEDKSGFTFOAALHHDGRIVFAYKEIPM 268
QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTP 300
Db 269 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSKVTSMSAVEFTP 328
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQ 360
Db 329 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRIYRQEWMDYGAQAEGRMCEDFQ 388
QY 361 DEDHDSASPD 371
Db 389 DEDHDSASPD 399
RESULT 12
US-10-284-237-2453
; Sequence 2453, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131PI1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2453
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC_FEATURE
LOCATION: (135)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (141)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2453

Query Match 26.0%; Score 130; DB 6; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 MDYCAQFAEGRMCEQDEHDHDSASPTSPYDGDLLTTSSSLFDTSLTTEDDTKLN 402
Db 1 MDYCAQFAEGRMCEQDEHDHDSASPTSPYDGDLLTTSSSLFDTSLTTEDDTKLN 60
QY 403 YAGDGLQNNLSPTKGTGPHLGTIVGIVLAVLLVAAILAGIYINGHPTSNALFFIER 462
Db 61 YAGDGLQNNLSPTKGTGPHLGTIVGIVLAVLLVAAILAGIYINGHPTSNALFFIER 120
QY 463 RPHHPAMKF 472
Db 121 RPHHPAMKF 130

RESULT 13
US-10-266-252-7
Sequence 7, Application US/10266252
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Ren, Feiyan
TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like Polypeptides and Polynucleotides and Therapeutic Uses Thereof
FILE REFERENCE: HYS-44A
CURRENT APPLICATION NUMBER: US/10/266,252
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/327,731
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/127,636
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 18
TYPE: PRT
ORGANISM: homo sapiens
US-10-266-252-7

Query Match 3.6%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARA 18

Db 1 MRGELWLLVLRRAARA 18
RESULT 14
US-10-266-252-13
Sequence 13, Application US/10266252
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Ren, Feiyan
TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like Polypeptides and Polynucleotides and Therapeutic Uses Thereof
FILE REFERENCE: HYS-44A
CURRENT APPLICATION NUMBER: US/10/266,252
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/327,731
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 17
TYPE: PRT
ORGANISM: homo sapiens
US-10-266-252-13

Query Match 3.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 IVGIVLAVLLVAAILA 443
Db 1 IVGIVLAVLLVAAILA 17

RESULT 15
US-10-218-140-526
Sequence 526, Application US/10218140
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/127,728
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/127,636
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/127,607
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 6322
SOFTWARE: Curanator Version 1.0
SEQ ID NO 526
LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-140-526

Query Match 2.0%; Score 10; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146

Db 161 LSFDFPYGH 170
|||||

Search completed: April 22, 2003, 16:24:15
Job time : 101 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:04:50 ; Search time 21 Seconds
(without alignments)
2288.915 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLVLRRAALS.....YAEVPSGHEKEGFMABQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	22.7	476	2 T19786	hypothetical prote
2	126	4.7	1161	1 S31213	nidogen precursor
3	115.5	4.3	1568	2 T09074	semaphorin recepto
4	103.5	3.8	979	2 C86446	probable cellulose
5	101.5	3.8	743	2 T09173	EH domain protein
6	101	3.8	733	2 E86345	hypothetical prote
7	100	3.7	535	2 S18606	phosphoenolpyruvat
8	99	3.7	1133	2 T12529	hypothetical prote
9	98	3.6	345	2 T16074	hypothetical prote
10	98	3.6	1502	2 S45429	probable membrane
11	97	3.6	707	2 I83196	NEDD-4 ORF - mouse
12	96.5	3.6	398	2 S33415	corticosteroid-bin
13	96.5	3.6	679	2 T19703	hypothetical prote
14	95.5	3.5	399	1 S71480	homeotic protein H
15	95.5	3.5	887	2 S70642	ubiquitin ligase N
16	95.5	3.5	2120	2 T30243	alpha tectorin - C
17	94	3.5	774	2 JC7265	neprilysin (EC 3.4
18	93.5	3.5	979	1 JC2349	protein-tyrosine-p
19	93.5	3.5	996	2 T48721	ptp 35 protein - m
20	93.5	3.5	1977	2 S54771	sodium channel alp
21	93	3.5	491	2 AG3506	phosphoenolpyruvat
22	93	3.5	1085	2 S55332	IFH1 protein - yea
23	92.5	3.4	441	2 JC7653	pectate lyase (EC
24	92.5	3.4	852	2 A85041	probable receptor
25	91.5	3.4	614	2 A98241	hypothetical prote
26	91.5	3.4	614	2 F86088	hypothetical prote
27	91.5	3.4	810	1 P2WMBB	2a protein - broad
28	91.5	3.4	1042	2 A57534	mucin 5AC (clone L
29	91	3.4	633	2 S47144	mating type A prot

RESULT 1

T19786

hypothetical protein C36E8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T19786

R:Wilkinson, J.: Barlow, K.

submitted to the EMBL Data Library, August 1994

A:Reference number: Z19177

A:Accession: T19786

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-476 <WIL>

A:Cross-references: EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C36E8.3

A:Experimental source: clone C36E8

C:Genetics:

A:Gene: CESP:C36E8.3

A:Map position: 3

A:Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2

C:Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 22.7%; Score 611; DB 2; Length 476;
Best Local Similarity 34.2%; Pred. No. 3.7e-42;
Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;

QY	46	RRARESPGHVSEPDRTOLS-----QDLGGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPS	100
DB	62	RTARAAP-----IPKRSLSAEQDEDEIDPATATIP--PDVEKNDMDHQYQAEFTVGD	115
QY	101	EPHSRELWVDVAEANSQVKI-----HTILSNTHRQASRVVLSPDFFYGHPLRQITITATG	156
DB	116	GETLKWYINVEQFMKKPRAVGNTPHLLSQSYRRAVGARLQFKPFYGHKNSNLTATG	175
QY	157	GFIFMGDVIHRMLTATQYVAPLANENPGYSDNSTVYVDNGTVFVQNDHVYLOGWEK	216
DB	176	GFYIGDHSNHLAAATQYIAPLANFHT--YLNNSNIVYADGELFVVEWRNVOLKEDKDE	234
QY	217	GSFTQAAALHDKGRVIFAYKEIPMSVPEISSQHPVKTKGLSDAFMLN--PSPDVPESRR	274
DB	235	HSFTFTILKHGNDIVFIYKDPYDINSIDANHPVKLGISDAYMFKHNLHQAAP--K	291
QY	275	RSIFEXHRIELDFSKVTMSAVETFTPLPTCLQHRSCDACMSDLT-FNCSWCHVLQR---	330
DB	292	RVIVYEHRIEIAQAQKIVSNWTWILKAQPTCISFDTCTNATLPHFNCILWCHAKKSHGG	351
QY	331	--CS--SGFDRYQEWMDYGCAGAEGRMCE-DFQEDDHDSAS-PDTSFSPYDGLTITS	384
DB	352	PFCTDEAGLHRRRHQWFEQNGYQSRKALYCDADDEDEYDEEDYPKSQLMPNGGH---	408
QY	385	SSLFIDSILTTEDDTKLPYAGGDCGLQNNLSPKTKGTPVHLGTIVGIVLAVLLVAAILAG	444
DB	409	LPLDADRMKTKDTKTSSEDSDEWKGHKKEEPK-----GG	442

protein-tyrosine-p
pregnancy-specific
zona pellucida gly
pristinamycin I sy
phosphoenolpyruvat
phosphoenolpyruvat
hypothetical prote
protein tyrosine p
hypothetical prote
hypothetical prote
protein-tyrosine k
Doc4 protein, stre
pregnancy-specific
osteonidogen - hum
probable polyketid
sodium channel pro

QY 445 IYINGHP--TSNAALF 458
 : : : : :
 Db 443 VATTAPVGTQAATF 458

RESULT 2

S31213

nidogen precursor - sea squirt (Halocynthia roretzi)

N:Alternate names: entactin

C:Species: Halocynthia roretzi

C:Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000

C:Accession: S31213

R:Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.

Eur. J. Biochem. 213, 11-19, 1993

A:Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of

A:Reference number: S31213; MUID:93238676; PMID:8477687

A:Accession: S31213

A:Molecule type: mRNA

A:Residues: 1-1161 <NAK>

C:Superfamily: EMBL:D14038; NID:g217363; PIDN:BAA03127.1; PID:g217364

C:Keywords: Ascidian nidogen; EGF homology; LDL receptor WYTD-containing repeat homol

F:1-20/Domain: basement membrane; collagen binding; disulfide bond; duplication; extracellu

F:21-1161/Product: nidogen #status predicted <SIG>

F:274-306/Domain: EGF homology <EGL>

F:560-574/Region: 3-residue repeats (R-P-V)

F:603-673/Domain: thyroglobulin type I repeat homology <THY1>

F:686-748/Domain: thyroglobulin type I repeat homology <THY2>

F:752-819/Domain: thyroglobulin type I repeat homology <THY3>

F:900-943/Domain: LDL receptor WYTD-containing repeat homology <YWL>

F:944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>

F:987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>

F:1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>

F:1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW5>

F:1119-1158/Domain: EGF homology <EG2>

F:1107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 4.7%; Score 126; DB 1; Length 1161;

Matches 64; Conservative 34; Mismatches 88; Indels 86; Gaps 12;

QY 137 LSFDPFPYGHPLRQITATGGFIEN-----GDVIRHMLTATQYVAPLMAN----- 181

Db 47 LSPMTVFYDQYKYSVTHTDGFITLNVGADTDGEVL-----LAPFMSDLDTLSG 97

QY 182 --FNPFGSDNSTVY-----FDNCTVFVQWDHVVYLGWEDKGSFTFQAA 224

Db 98 DIFPREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKVQSASREDGVFTFQCI 157

QY 225 LHHDRIVFA---YKEIPMSVPEIS---SSQHPVKTGLSDA---FMILNPSF---DV 269

Db 158 VATGAATFAFLYPQGLAVGENAVKGVNREVTARAGFNDGGREQLLELSADELIGGDN 217

QY 270 PESRRSIFVHRIELDPSKVTMSAVEFTPLPTCLQHRSCDACMSSDITFNCISWCHVLQ 329

Db 218 AGSOGQWIFQIGLIMFNDEASKESK-----KH-----HVKK 249

QY 330 RCSSEDFRYQEW-MDYCCQAQAE-GRMCEDF 359

Db 250 TRQSGFQVQSVNFDNFIDLEACGPPCSDF 281

RESULT 3

T09074

semaphorin receptor VESPR - human

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T09074

R:ComEAU, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; F

Immunity 8, 473-482, 1998

A:Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and b

A:Reference number: Z16555; MUID:98246049; PMID:9586637

A:Accession: T09074

A:Status: preliminary; translated from GB/EMBL/DDBI

A:Molecule type: mRNA

A:Residues: 1-1568 <COM>

A:Cross-references: EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3176762

A:Experimental source: tissue type foreskin; cell type fibroblast

C:Genetics:

A:Gene: VESPR

C:Keywords: receptor; signal transduction

Query Match 4.3%; Score 115.5; DB 2; Length 1568;

Best Local Similarity 20.6%; Pred. No. 0.98;

Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

QY 39 GTVRGWNRARRSPGHVSEPDRT---QLSODLGGGTLMADTLPDNRTRVEDNHSYVVS 94

Db 256 GAATGWPSPMAR-----TAQSTEVLFQOQASLDCGHGH-----PDGR-----R 292

QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139

Db 293 LLLSSSLVEALDVMAGVFSAAAGEGOERRSPPTTALCLFMSIQARXVSWDFKTAES 352

QY 140 ----DFPFYGHPLRQITATGGFIEMGDIHRLMTATQYVAPLMANFNGYSDNSTVYV 194

Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391

QY 195 FDNCTVFVQWDHVVYLGWEDKGSFTFQAAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249

Db 392 LGTG-----DGQLKVLIGENLTSNCPEVIVEIKEE 422

QY 250 HPVKTGLSDFAMLLNPSDPVPSRRRSIFEYHRIELDPKVTMSAVEFTPLPTCLOHRS 309

Db 423 TPV-----FYKLVPDP-----VKNYIY-----LTAGREVRRIRVANCKHKHS 460

QY 310 CDACMSDLTENCSCWCHVLRQCSGDFDRYQE---WMDYGCQAQAEGRMCEDFQ----D 361

Db 461 CSECLTA-TDPCGCHSCLQRTFCQDGVHSENLENWLDI-----SSGAKKCPKIQIRSS 515

QY 362 EDHDSASPDTSFSP 375

Db 516 KEKTTVTVMVGSFSP 529

RESULT 4

C86446

probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001.#sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C86446

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Liu, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C86446

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-979 <STO>

A:Cross-references: GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 3.8%; Score 103.5; DB 2; Length 979;

Best Local Similarity 21.2%; Pred. No. 5;

Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;

QY 4 ELWLLVLVLRRAARALSPPGAGHDGPGCGAAKGTVRGNRRRARESPGHVSEPDRTQL 63

Db 342 EKXKHKVYVEDQIKERPAL---VAPKATWMSDGT---HWPGTWAVSGPHHSRGDHSV 396
QY 64 SDDL-----GGGTAMD-----TLPNRTRVVEDNHSYVSRLYGPSEPHSR 105
Db 397 IOVLDPGPDPEVEGKGGRALDLEGVDIRLP-----MLVYVSRREKRPYDHNN 446
QY 106 ELWVDVAENRSOVKIHITLSTHNRQASRVLSFDPPYGHPLQITATIGGTFPMGDVI 165
Db 447 K-----AGAMNALVRASATMSN-----GPFILNDCDHVYNSRAF-----ROGICFMDHD 493
QY 166 HRMLTATQY-----VAPLMANFNPGYSD-----NSTVYV-F 195
Db 494 GDRSVYVQPPQFEGIDFSRDYANKNTVFEDINLRALDIOGPMYVGTGCLFRRTALYGF 553
QY 196 DNGTFVYVQWHDVHYLOQWEDKSGFTFOALHHDGRIVFAYKEIPMSV---PEISSQHP- 251
Db 554 NPPDVVFE-----EPPSGYCFP-----LIKKRSPATVASEPEYTYDEDR 595
QY 252 -----VKTGLSDAFMLNPSDPVPSRRSIFEXH--RIELDPSKVT-SMSAVEFTPLPT 303
Db 596 FIDGIRKQFGSSMLVN-SVKVAEFGRLPLATVHSSRLGRPPGSLTGSRLPLDFATVNE 654
QY 304 CLQHRSCDACMSDITFNCISWCH--VLQRCSSGFDYRQEWMDYCAQAEAE 352
Db 655 AVNVISCWYEDKTENGFGVNGWYIGSVTDVYTGFRMHEKGWRSFYCVTEPD 705
RESULT 5
T09173
EH domain protein Reps1 - mouse
N:Alternate names: RalBP1-associated EH domain protein Reps1
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09173
R:Yamaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.
J. Biol. Chem. 272, 31230-31234, 1997
A:Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1
A:Reference number: Z16602; MUID:98058900; PMID:9395447
A:Accession: T09173
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-743 <YAM>
A:Cross-references: EMBL:AF031939; NID:q2677842; PIDN:AAB94736.1; PID:q2677843
A:Experimental source: cell line: C2C12; tissue type: muscle
C:Genetics:
A:Gene: rep1
C:Keywords: signal transduction

Query Match 3.8%; Score 101.5; DB 2; Length 743;
Best Local Similarity 18.3%; Pred. No. 4.9; Mismatches 166; Indels 177; Gaps 23;
Matches 91; Conservative 63;
QY 19 LSPQAGH-DEGPGSGMAK-----GTVGRNRRARESPGHV 55
Db 78 IPPPGRGVKKGGSHDAVQPPSAEQEPASPVVSPQSPPTSPHTWKHSRHPSGN 137
QY 56 SEDPTQLSQ-----DLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGPSPHRELMV 109
Db 138 SERPLTGPFPWFSPFGDAQAGSAGDAV-----WSQSPPPPPQDNMV 179
QY 110 DVAF-----ANRSOVKIHITLS-NTHQASRVLSFDPPYGHPLQITAT 155
Db 180 SFADTPTTSALLTMHSPASVODQTVTVASATAFANIRQSSYEDPW-----KITDB- 232
QY 156 GGFIFMGDVTHRMILTATQY--VAPLMANFNPGYSDNSTVYVFDNGTFVYVQWHDVY-LOG 212
Db 233 -----QRQYVYVQKTIQDPLNGFTPG---SAAKEFTKSKLPILSLSHIWLSD 279
QY 213 WEDKGSFT---FOALHHDGRIVFAYK---EIPMSVPEITSSSSOHPHVKTKGLSDAFMLNPS 266
Db 280 FDKDGLTLDLFECAAFH---LVVARKNGYDLPEKLPE-----SLMPKLLIDLEDS 325

QY 267 PDVPESRRRSIFEYHRIELDPKSVTSMASVEFTPLTCLQHRSCDACMSDITFNCISWCH 326
Db 326 ADVGEQGEVGYSGSFAEAPPSPSPSL-----NOTWPE 361
QY 327 VLQRCSSGFDYRQEWMDYCAQAEAGRMCEDEQDEHDSASDPTS----- 372
Db 362 LNQS-----SEQWETFS-ERSSSQTLTQF-DSNIAPADPDATIAVHPVPIRMTPSKI 411
QY 373 -----FSPYDGLTITSSSLFIDSLTTEDDTKLP-----VAGDGLONNLS 414
Db 412 HMOEMELKRTSSDHTNTPSLLVKPSDLSEENKINSVKRPPSGNTVDGYSSDSFFSD-- 469
QY 415 PKTKGTPV-----HLGT 426
Db 470 PEQIGSSVTRQSRHSGT 486
RESULT 6
E86345
hypothetical protein F16F4.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86345
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talbot, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-733 <SPO>
A:Cross-references: GB:AE005172; NID:g8920637; PIDN:AAF81359.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; p

Query Match 3.8%; Score 101; DB 2; Length 733;
Best Local Similarity 24.1%; Pred. No. 5.3;
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;
QY 257 SDAFMLNPSDPVPSRRRSI-----FEYHRIELDPKSVTSMASVE-FTPLPTCL 305
Db 139 STGCMSLCDTTPPPNSKNGVGCRCRTEVSIPLDSHRIETQPSRFENMTSVEHNP----- 193
QY 306 QHRSCD-ACMSDITFNC-----WCVLQRC-----SS 333
Db 194 ----CSVAFFYEDGMENFSSLEDLKLNRNTRFPVLLDWSIGNOTCEQVYVGRNITCGNST 249
QY 334 GFDRYRQSBMDYCAQAEAGRM-----CEDFOD---EDHDSASPD-----SF---SPY 376
Db 250 CFDRTRGKYCKKLOQFDGNPYLSDGCODECTRIHNCSDTSTCENTLGSFHCQCP 309
QY 377 DGLTITSSSLFIDSLATEDDTKLNXPYAGDGLONNLSPKTKG-TPVHLGTIVGIVLAVL 435
Db 310 GSDLNTTMSG- IDTPKEE-----PKYLGWTTVLGGTTIGFLILL 349
QY 436 LVAAT 440
Db 350 TISYI 354
RESULT 7
SI8606
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.
C:Species: Rhizobium sp.
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001

A;Cross-references: EMBL:X79489; NID:g496661; PID:g496702

A;Title: Identification of a set of genes with developmentally down-regulated expression in the developing mouse brain.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992

S.; Tomooka, Y.; Noda, M. Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992

Accession: 105130
R; Kumar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992.

Accession: Q15740
A; Molecule type: protein
A; Residues: 23-40 <SCR2>

A;Molecule type: protein
A;Residues: 23-40 <SCR2>
C;Superfamily: antithrombin

C:Keywords: glycoprotein; steroid binding
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-397/Product: corticosteroid-binding globulin #status experimental <MAT>
F:89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.68; Score 96.5; DB 2; Length 397;
Best Local Similarity 20.28; Pred. No. 5.3;
Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;

QY 61 TQLSODLGGTGLTMDTLPDNRTRVVDNHSYVSRKLYGSPSEPHSRRLWVDVAE-----A 114
DB 114 TGLENNWVFLQNLKDKFLADKHYEALIPSKD-----WTAGEGINNHVK 168
QY 115 NRSQVKIHILSNTHROASRVLSDFE-----PFYGHPLRQTITATGFIPIGMDVIHR 167
DB 169 NKTQKIEHVYVSDLDSSATLILINIELKGIWKLFPSPENTRE-----EDFYV 216
QY 168 MLTATQVYVAPLMAFNFCYSDNSVTV-----YFDNGTVFVQWDHVIYLOGWEDKGSFT 220
DB 217 NETSTVKPMVQSGNISYFRDSAIPQVMQVNGTTFIILPD-----QGQMD-----T 268
QY 221 FQAALHHD-----GRIVFAYKEIPMSVEISSQH-----PVKTGLSDAFMILNFSPOV 269
DB 269 VVAALNRDTIDRWGKLMIP-RQMNLYIPKFSMSDYDLQDVLDVGIKDLFTQSDPADT 327
QY 270 PESRRRSIFEYHR--IELDPSKV 290
DB 328 TKDTPLTTLTVLHKAMQLQDEGNV 350

RESULT 13

T19703

hypothetical protein C34C12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19703

R:Kershaw, J.

submitted to the EMBL Data Library, December 1994

A:Reference number: Z19166

A:Accession: T19703

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-679 <WIL>

A:Cross-references: EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C34C12.2

A:Experimental source: clone C34C12

C:Genetics:

A:Gene: CESP:C34C12.2

A:Map position: 3

A:Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3

Query Match 3.68; Score 96.5; DB 2; Length 679;
Best Local Similarity 23.38; Pred. No. 11;
Matches 70; Conservative 36; Mismatches 130; Indels 65; Gaps 12;

QY 16 ARALSPQAGHDEGGCGGWAAGTVRGWNRRARESPGHVSEPDRTQLSODLGGGTAMD 75
DB 337 AKYLKPDQPTSSACYKPYFESTSSSRKPTASPG---PPGTQISDQLNTGEVRY- 392
QY 76 TLPDNRTRVVDNHSYVSRKLYGSPSEPHSRRLWVDVAEANRSQ---VKIHTILSNTHROA 132
DB 393 -----VNSGKPFNFS-----SESNRNLKIPYIKRPFERYIKPEGFTSASYKQAQ 439
QY 133 SRVLSDFDFPYGHPLRQITAT-----GGFTFMGDVTHRMCTATQYVAPLMAFNFCY 186
DB 440 SEGMSFP-----LKTGSATPENSCKSAHDFMDPI-----SSTPYKSHVVVSEDMN 486
QY 187 SDNSTVYVF-----DNGTVFVQWDHVIYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMS 241
DB 487 SSSSTGGFSEKDKNGAL-----GSQKSPMPDIATALHN-----IFDSKEVQSS 531
QY 242 VPEISSSQHVPTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVKTSMSAVEFTPL 301
DB 532 SSTTGSAPPENSKSDHF-----DMPDISSTLYRSRVE--PISSSSGSGTSTISAPRYVPK 585

QY 302 P 302
DB 586 P 586

RESULT 14

S71480

homeotic protein Hox B3 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S71480

R:Scotting, P.J.; Rex, M.

submitted to the EMBL Data Library, August 1993

A:Reference number: S71480

A:Accession: S71480

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-399 <SCO>

A:Cross-references: EMBL:X74506; NID:G398704; PIDN:CAA52613.1; PID:G443794

C:Genetics:

A:Gene: Hox-B3

C:Superfamily: homeotic protein Hox B3; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:160-216/Domain: homeobox homology <HOX>

Query Match 3.58; Score 95.5; DB 1; Length 399;
Best Local Similarity 20.58; Pred. No. 6.5;
Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;

QY 246 SSSQHPVKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMS-----AVEFT 299
DB 94 STSSNISPGSAKVPKPTSVQTP-SLTQKIFPMKESRQNSKOKSSPSTETCSGEKT 152
QY 300 PLPTCLQHRSCDACWSSDLT-----FNCWCH-----VLQRCSSGFDRYRQEW-----M 343
DB 153 PPGSASRKRATAYTSAQLVELEKEFHFNLCRRPRRVEAMNLLNSLRQIKIMFQNRMM 212
QY 344 DYGCAQAEGRMCEDEFDEHDSASPDTSFSP-----VDGLTFTTSSSLFTDSLTT 394
DB 213 KYKDKQSKGM-----GSSSGGSPSTGPPQPMQSGAGFMALHTMSSNYDAPSPS 264
QY 395 EDTKLNIPYAGDGLQNNL-----SPKTKGTPVHLGT 426
DB 265 LNKPHQAYAHVTNYQNPDKGALQOKYNTAPEYDPHVLOGNVAYGTPSMQSGSPVYVG- 323
QY 427 IVGIVLAVLLAAIILAGIYINGHPTSNAAIFFIERRRHHWPAKFRSHPDHSYAEVPE 486
DB 324 -----GNVDSLPTSGPSLYGLNHLPHHQA-----NMDYSGPPQMP 361

QY 487 SGH 489

DB 362 SQH 364

RESULT 15

S70642

ubiquitin ligase Nedd4 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000

C:Accession: S70642

R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

EMBO J. 15, 2371-2380, 1996

A:Title: WW domains of nedd4 bind to the proline-rich PY motifs in the epithelial Na(

A:Reference number: S70642; MUID:96221297; PMID:8665844

A:Accession: S70642

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-887 <STA>

A:Cross-references: EMBL:U50842; NID:G1293646; PIDN:AAB48949.i; PID:G1293647

C:Genetics:

A:Gene: Nedd4

C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubi

F:54-167/Domain: protein kinase C C2 region homology <KC2>
F:246-283/Domain: WW repeat homology <WW1>
F:402-439/Domain: WW repeat homology <WW2>
F:459-496/Domain: WW repeat homology <WW3>
F:555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 3.5%; Score 95.5; DB 2; Length 887;
Best Local Similarity 19.2%; Pred. No. 20;
Matches 93; Conservative 55; Mismatches 155; Indels 181; Gaps 25;

QY	14	EAARALSP-----QPGAG-----HDEGPG-----SGMAAKGTVRG-----WNRR	47
Db	218	DOAELEFGVVLDPDAATHLQHPPEPLPPGWEERQDVLGRYYVNVNHSRTQWKR	277
QY	48	ARES-----PGHVSEPORTQLSODLGGTTLAMDITLNDNTR-----VVEDNH	89
Db	278	SPEDDLTDENGDIQLQAHGAFTRRQISEVDG-----PDNHPENWEIVREDEN	329
QY	90	SYVSR-LYGFSEPHSRELWVDAEANKRSQVKIHTILSNTHRQASRVVLSDFPFYGHPL	148
Db	330	TIYSQAVQSPSPCHP-DVQVRLAE-----ELDTRLT-----MYGNPA	366
QY	149	ROITATGGFTFMGDVIRMLTATQYVAPLM-----ANENPGY-----SDNSTVYFDNGTV	200
Db	367	TSQPVTSNHSRSGSSQTCIFEQPTLPVLLPTSSGLPPGWEERQDDGRGRSYVDHNSK	426
QY	201	FVQWDHVVLQ-----GWEDKGSFTFQAALHHDGRIVF	233
Db	427	TTTWSKPTMQDDPRSKIPAHLRGKTPVDSNDLGLPLPGWEER-----THTDGRVFF	477
QY	234	AYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESR-RRSIFEYHRIELDPKSVTS	292
Db	478	INHNIKKTQWEDPRMQNVAITG-----PAEPYSRDYKRKYEFERKLLKKQ----	522
QY	293	MSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRIYQREWMDYGCQAQAE	352
Db	523	TDIPNKFEMK-----LRRANILEDYSYRR-IMGVRRADFLK	556
QY	353	GRMCEDFODE---DHDSASPD-----TSFSPYDGLTTTSSSLFIDSLTDEDT-KLN	401
Db	557	ARLWIEFDGCKLDYGGVAREWFFLLISKEMFNPPYG-----LFEYSATEDNWTLOIN	608
QY	402	PYAG	405
Db	609	PNSG	612

Search completed: April 22, 2003, 16:08:19
Job time : 26 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:14:56 ; Search time 45 Seconds

(without alignments)
1068.160 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

Sequence: 1 MRCELWLLVLRARALS.....YAEVPSGHEKGFMEARQC 500

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR.73.*

1: pirl.*

2: pirl.*

3: pirl.*

4: pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.8	655	2 E69791	conserved hypotet
2	8	1.6	224	2 T36146	hypothetical prote
3	8	1.6	317	2 T30232	methyitransferase
4	8	1.6	363	2 E84280	hypothetical prote
5	8	1.6	429	1 C41903	arsenical pump mem
6	8	1.6	472	2 E81817	probable sodium/al
7	8	1.6	472	2 F81058	amino acid symport
8	8	1.6	476	2 T19786	hypothetical prote
9	8	1.6	483	2 T35715	export protein - S
10	8	1.6	562	2 A12507	hypothetical prote
11	8	1.6	751	2 T46517	hypothetical prote
12	7	1.4	75	1 W5WL33	E5 protein - human
13	7	1.4	76	1 W5WL58	E5 protein - human
14	7	1.4	78	2 S08449	hypothetical prote
15	7	1.4	82	2 G97758	hypothetical prote
16	7	1.4	100	2 A43998	hypothetical prote
17	7	1.4	106	2 JQ1248	hypothetical 12K p
18	7	1.4	114	2 T08325	hypothetical prote
19	7	1.4	131	2 T01293	hypothetical prote
20	7	1.4	133	2 A97192	hypothetical prote
21	7	1.4	147	2 A00539	hypothetical prote
22	7	1.4	150	2 F87589	hypothetical prote
23	7	1.4	154	2 AD3475	protein-Npi-phosph
24	7	1.4	166	2 F97128	probable membrane
25	7	1.4	170	2 F87482	hypothetical prote
26	7	1.4	177	2 F87600	conserved hypotet
27	7	1.4	178	2 E75340	conserved hypotet
28	7	1.4	186	2 F97395	modulation protein
29	7	1.4	186	2 AH2613	modulation protein

hypothetical prote
capsular polysacch
conserved hypotet
E1 membrane glycop
E1 membrane glycop
E1 membrane glycop
E1 membrane glycop
hypothetical prote
probable integral
probable transcrip
conserved hypotet
probable membrane
hypothetical 30.5K
moac protein [impo
probable [imported
F24J8.7 protein -
probable transport
iron(III) dicitrat
hypothetical prote
cytochrome c-type
hypothetical prote
transcription regu
ribose transport s
LacI-family trans
probable ABC trans
probable integral
probable carboxyno
invasion protein i
cell invasion prot
probable cytochrom
cell division prot
probable rod shape
hypothetical prote
protein secretion
imidazoleprocton
conserved hypotet
sodium/glutamate s
heat shock protein
heat shock protein
heat shock protein
colligin-2 - human
hypothetical prote
Spa47 protein - Sh
uracil permease Ur
probable CDP-4-ket
diacylglycerol O-a
probable secretion
hypothetical prote
hypothetical prote
hypothetical prote
probable type II s
dihydropolipamide d
microsome-associat
probable imidazole
cannabinoide recept
hypothetical prote
L-xylokinase (EC
L-xylokinase (EC
conserved hypotet
probable integral
diacylglycerol O-a
hypothetical prote
acetyl-CoA/acetac
probable chemotaxi
Na+ ATPase chain J
NAD-diphthamide AD
NAD-diphthamide AD
probable ATP-bindi
cytochrome-c oxida
heat shock protein
dnak-type molecula
hypothetical prote

103	7	1.4	622	2	S57684	protable membrane	176	6	1.2	100	1	S27016	defensin alpha-6 p
104	7	1.4	627	2	A99607	hypothetical prote	177	6	1.2	100	2	B28487	apolipoprotein C-I
105	7	1.4	630	2	T31017	hypothetical prote	178	6	1.2	100	2	G87478	hypothetical prote
106	7	1.4	643	2	E82481	methyl-accepting c	179	6	1.2	102	2	F69475	conserved hypoteth
107	7	1.4	660	1	A54942	acyl-CoA oxidase (180	6	1.2	102	2	G96775	hypothetical prote
108	7	1.4	660	1	B54942	acyl-CoA oxidase (181	6	1.2	102	2	S50936	probable membrane
109	7	1.4	660	2	I38095	hypothetical prote	182	6	1.2	104	2	B82294	hypothetical prote
110	7	1.4	662	2	T17211	hypothetical prote	183	6	1.2	105	2	AD2301	hypothetical prote
111	7	1.4	693	1	S38427	NADPH-ferrihemopro	184	6	1.2	108	2	J01428	hypothetical 11.6K
112	7	1.4	704	2	T03478	probable DNA-direc	185	6	1.2	109	2	B9806	conserved hypoteth
113	7	1.4	723	2	AG3555	histidine ammonia-	186	6	1.2	109	2	T29123	hypothetical prote
114	7	1.4	751	2	T01449	cytoskeletal prote	187	6	1.2	110	2	B69227	hypothetical prote
115	7	1.4	763	2	F96693	hypothetical prote	188	6	1.2	110	2	D72673	hypothetical prote
116	7	1.4	769	2	E97092	glycosyltransferas	189	6	1.2	110	2	A82194	hypothetical prote
117	7	1.4	773	2	E97071	protein containing	190	6	1.2	110	2	A33934	hypothetical prote
118	7	1.4	794	2	I59372	cadherin 12 - huma	191	6	1.2	111	2	S27005	sporozoite surface
119	7	1.4	885	2	B69783	transporter homolo	192	6	1.2	111	2	S27005	dnak-type molecula
120	7	1.4	891	2	A97718	hypothetical prote	193	6	1.2	111	2	A58866	hypothetical prote
121	7	1.4	953	2	S75285	methyl-accepting c	194	6	1.2	111	2	AE0794	probable membrane
122	7	1.4	999	2	T36021	probable zinc-bind	195	6	1.2	114	2	B34792	Ig heavy chain pre
123	7	1.4	1014	2	T31433	Na+/Ca2+, K+-exchan	196	6	1.2	115	2	G87300	dihydroneopterin a
124	7	1.4	1065	2	A70797	hypothetical prote	197	6	1.2	116	2	H90966	hypothetical prote
125	7	1.4	1092	2	S42798	Na+/Ca2+, K+-exchan	198	6	1.2	117	2	T07864	germination-specif
126	7	1.4	1096	2	C87263	fibronectin-bindin	199	6	1.2	118	2	S45680	lipid transfer pro
127	7	1.4	1120	2	S46111	hypothetical prote	200	6	1.2	118	2	C84806	probable nonspecif
128	7	1.4	1172	2	S32689	probable membrane	201	6	1.2	119	2	C81821	probable integral
129	7	1.4	1184	2	T09484	paraspinal crystal	202	6	1.2	120	2	C91027	D-erythro-7,8-dihy
130	7	1.4	1199	2	S20969	cartilage intermed	203	6	1.2	120	2	D85871	D-erythro-7,8-dihy
131	7	1.4	1245	2	T42920	Na+/Ca2+, K+-exchan	204	6	1.2	120	2	E65002	D-erythro-7,8-dihy
132	7	1.4	1308	2	B75198	hypothetical prote	205	6	1.2	120	2	T17514	hypothetical prote
133	7	1.4	1628	2	F86194	DNA helicase relat	206	6	1.2	121	2	B87648	hypothetical prote
134	7	1.4	2126	2	H70821	hypothetical prote	207	6	1.2	122	2	T01589	acyl carrier prote
135	7	1.4	2391	2	T18410	probable polyketid	208	6	1.2	122	2	B70764	hypothetical prote
136	7	1.4	3670	2	T36249	carbamoyl-phosphat	209	6	1.2	124	1	F6PMV4	vicilin, 14K compo
137	7	1.4	3944	2	T19997	CDA peptide synthet	210	6	1.2	124	2	H69520	conserved hypoteth
138	6	1.2	11	2	A61483	hypothetical prote	211	6	1.2	124	2	S76185	hypothetical prote
139	6	1.2	43	2	S23641	pyridoxal kinase (212	6	1.2	124	2	B84258	hypothetical prote
140	6	1.2	47	1	D32535	cytochrome-b5 redu	213	6	1.2	124	2	H89794	hypothetical prote
141	6	1.2	47	1	JQ0330	colicin E5 lysis p	214	6	1.2	126	2	T02351	probable acyl carr
142	6	1.2	47	1	S27395	colicin E5 lysis p	215	6	1.2	126	2	T02351	CB59 protein - bab
143	6	1.2	47	1	S49178	colicin E7 lysis p	216	6	1.2	126	2	S75413	hypothetical prote
144	6	1.2	48	2	D89788	colicin E4 lysis p	217	6	1.2	126	2	T31972	hypothetical prote
145	6	1.2	55	2	B82375	hypothetical prote	218	6	1.2	127	2	B64034	hypothetical prote
146	6	1.2	66	2	S03443	dnak-type molecula	219	6	1.2	127	2	G82038	conserved hypoteth
147	6	1.2	68	2	S68975	tetrahydromethanop	220	6	1.2	128	1	S12372	spasmolytic protei
148	6	1.2	68	2	C69021	Ig heavy chain V-A	221	6	1.2	128	2	I36894	CB59 protein - gre
149	6	1.2	70	2	A30518	hypothetical prote	222	6	1.2	130	2	T29155	hypothetical prote
150	6	1.2	71	2	F69981	hypothetical prote	223	6	1.2	131	2	H82337	preprotein translo
151	6	1.2	74	2	AH1892	hypothetical prote	224	6	1.2	131	2	T02500	hypothetical prote
152	6	1.2	76	2	T36658	hypothetical prote	225	6	1.2	131	2	F71148	hypothetical prote
153	6	1.2	78	2	T17494	hypothetical prote	226	6	1.2	132	2	I47191	Ig heavy chain var
154	6	1.2	79	1	EV6CCF	sopC protein - Esc	227	6	1.2	132	2	T08676	hypothetical prote
155	6	1.2	80	2	E82500	hypothetical prote	228	6	1.2	134	2	B82768	hypothetical prote
156	6	1.2	81	2	B60396	antigen 7H8/1 - ma	229	6	1.2	134	2	A86475	virulence regulato
157	6	1.2	85	2	G86426	hypothetical prote	230	6	1.2	135	2	PN0527	15.8K F12A4.7 hypo
158	6	1.2	88	2	A84342	hypothetical prote	231	6	1.2	135	2	T35853	G protein-coupled
159	6	1.2	88	2	AG1356	hypothetical prote	232	6	1.2	135	2	F75137	probable oxidoredu
160	6	1.2	89	2	E82919	ribosomal protein	233	6	1.2	135	2	S52360	hypothetical prote
161	6	1.2	89	2	A81013	sugar transport pr	234	6	1.2	137	2	S52362	superoxide dismuta
162	6	1.2	89	2	F82757	hypothetical prote	235	6	1.2	137	2	S52365	superoxide dismuta
163	6	1.2	91	2	F69069	hypothetical prote	236	6	1.2	137	2	S52376	superoxide dismuta
164	6	1.2	93	2	C90192	conserved hypoteth	237	6	1.2	137	2	H83013	conserved hypoteth
165	6	1.2	93	2	H86472	probable 60S ribos	238	6	1.2	138	2	*H64064	ribulose-bisphosph
166	6	1.2	94	2	AC3342	hypothetical cytos	239	6	1.2	139	1	RKMLS	tolR protein - Hae
167	6	1.2	96	2	S49377	translation releas	240	6	1.2	139	2	H83663	hypothetical prote
168	6	1.2	96	2	AC1263	hypothetical prote	241	6	1.2	139	2	S38256	mannose-binding le
169	6	1.2	98	2	A11260	hypothetical prote	242	6	1.2	139	2	D86417	probable auxin-ind
170	6	1.2	98	2	S41562	hypothetical prote	243	6	1.2	140	2	S54227	Ig mu heavy chain
171	6	1.2	99	2	H75494	hypothetical prote	244	6	1.2	141	2	I47178	Ig heavy chain var
172	6	1.2	99	1	S28566	apolipoprotein C-I	245	6	1.2	141	2	H72540	hypothetical prote
173	6	1.2	99	2	S75918	probable ferredoxi	246	6	1.2	143	2	T20464	hypothetical prote
174	6	1.2	99	2	G97228	glu-TRNAGln amidot	247	6	1.2	144	2	T03563	probable ribosomal
175	6	1.2	99	2	B97837	(p)ppGpp 3-pyropho	248	6	1.2	144	2	C83633	hypothetical prote

249	6	1.2	145	2	S74292	hypothetical prote	322	6	1.2	162	2	T13574	NADH2 dehydrogenas
250	6	1.2	145	2	E84461	hypothetical prote	323	6	1.2	162	2	S75277	hypothetical prote
251	6	1.2	146	1	PSFGA	phospholipase A2 (324	6	1.2	163	2	G75424	bacterioferritin c
252	6	1.2	146	2	T25640	hypothetical prote	325	6	1.2	164	2	S48319	probable membrane
253	6	1.2	147	1	LZQJE	lysozyme (EC 3.2.1	326	6	1.2	165	2	C48232	cysteine-rich exte
254	6	1.2	147	2	H86851	hypothetical prote	327	6	1.2	165	2	G84508	hypothetical prote
255	6	1.2	147	2	B86699	hypothetical prote	328	6	1.2	166	2	F96786	protein F10A5.11 [
256	6	1.2	148	1	PSHU	phospholipase A2 (329	6	1.2	166	2	B72626	hypothetical prote
257	6	1.2	148	2	B72782	hypothetical prote	330	6	1.2	167	2	S20066	paracretic-type ri
258	6	1.2	148	2	T14784	hypothetical prote	331	6	1.2	167	2	H64444	hypothetical prote
259	6	1.2	149	2	F65169	ol149 protein - Esc	332	6	1.2	167	2	H83432	regulatory protein
260	6	1.2	149	2	B91206	hypothetical prote	333	6	1.2	168	2	S21041	cytochrome-c oxida
261	6	1.2	149	2	D86052	hypothetical prote	334	6	1.2	168	2	G71316	probable rod shape
262	6	1.2	149	2	E87344	ribonuclease P pro	335	6	1.2	168	2	B95330	hypothetical prote
263	6	1.2	149	2	F72677	hypothetical prote	336	6	1.2	170	2	F85093	hypothetical prote
264	6	1.2	150	1	NRBO	pancreatic ribonuc	337	6	1.2	172	2	B75338	thermoresistant gl
265	6	1.2	150	1	NRBOS	seminal ribonuclea	338	6	1.2	172	2	C69267	hypothetical prote
266	6	1.2	150	2	S43955	probable NADH2 deh	339	6	1.2	174	2	S01189	NADH2 dehydrogenas
267	6	1.2	150	2	S69530	hypothetical prote	340	6	1.2	175	2	B84828	hypothetical prote
268	6	1.2	151	2	A86695	hypothetical prote	341	6	1.2	176	2	B72004	shikimate kinase C
269	6	1.2	151	2	A12685	hypothetical prote	342	6	1.2	176	2	C86620	shikimate kinase I
270	6	1.2	151	2	AH1839	two-component syst	343	6	1.2	176	2	B81208	conserved hypothet
271	6	1.2	152	1	NRRT	pancreatic ribonuc	344	6	1.2	176	2	H75332	ankyrin-related pr
272	6	1.2	153	2	S17837	pancreatic ribonuc	345	6	1.2	177	2	A99606	hypothetical prote
273	6	1.2	153	2	S17837	sorbin - pig	346	6	1.2	177	2	T34292	FMRFamide-like pep
274	6	1.2	153	2	T09188	probable outer mem	347	6	1.2	178	2	A71512	hypothetical prote
275	6	1.2	154	2	F82633	probable protein d	348	6	1.2	178	2	C87677	hypothetical prote
276	6	1.2	156	2	A1036	probable lysozyme	349	6	1.2	179	2	S59503	ferric pseudobacti
277	6	1.2	156	2	A70968	hypothetical prote	350	6	1.2	180	2	AE1596	signal peptidase I
278	6	1.2	156	2	H72621	hypothetical prote	351	6	1.2	182	2	A02946	keratin, 59K type
279	6	1.2	157	2	A10927	probable lysozyme	352	6	1.2	182	2	S03259	methyl coenzyme M
280	6	1.2	157	2	D31327	IgE receptor alpha	353	6	1.2	182	2	T36728	probable DNA-bindi
281	6	1.2	157	2	S58014	probable olfactory	354	6	1.2	182	2	H82981	hypothetical prote
282	6	1.2	158	2	S37355	glutamate-ammonia	355	6	1.2	184	2	D87605	transcription regu
283	6	1.2	158	2	B95153	v-type sodium ATP	356	6	1.2	185	2	S73114	photosystem I chal
284	6	1.2	158	2	B69124	hypothetical prote	357	6	1.2	185	2	T07700	hypothetical prote
285	6	1.2	158	2	T14078	hypothetical prote	358	6	1.2	185	2	T49660	glucan 1,4-alpha-g
286	6	1.2	158	2	C86937	probable membrane	359	6	1.2	185	2	B97933	conserved hypothet
287	6	1.2	159	2	S40727	hypothetical prote	360	6	1.2	186	2	C72782	hypothetical prote
288	6	1.2	160	2	T17048	NADH2 dehydrogenas	361	6	1.2	189	1	G69355	hypothetical prote
289	6	1.2	160	2	C89832	hypothetical prote	362	6	1.2	189	1	B69040	probable 3-isoprop
290	6	1.2	160	2	A82214	hypothetical prote	363	6	1.2	189	2	A71569	hypothetical prote
291	6	1.2	161	2	A45000	peptidylprolyl iso	364	6	1.2	190	1	KLSSAA	calcium-binding pr
292	6	1.2	161	2	E48232	cysteine-rich exte	365	6	1.2	190	2	T10968	hypothetical prote
293	6	1.2	161	2	D81940	probable membrane	366	6	1.2	190	2	B83690	hypothetical prote
294	6	1.2	161	2	E81166	hypothetical prote	367	6	1.2	191	2	G87253	hypothetical prote
295	6	1.2	161	2	F69338	hypothetical prote	368	6	1.2	192	1	KLSSAB	calcium-binding pr
296	6	1.2	162	1	CFMWA	C-phycocyanin alph	369	6	1.2	192	2	T41413	thioredoxin peroxi
297	6	1.2	162	2	T10745	NADH2 dehydrogenas	370	6	1.2	192	2	C71543	probable phenylacr
298	6	1.2	162	2	T17047	NADH2 dehydrogenas	371	6	1.2	192	2	T37657	hypothetical prote
299	6	1.2	162	2	T17045	NADH2 dehydrogenas	372	6	1.2	192	2	A84727	hypothetical prote
300	6	1.2	162	2	T13487	NADH2 dehydrogenas	373	6	1.2	192	2	F71169	hypothetical prote
301	6	1.2	162	2	T14256	NADH2 dehydrogenas	374	6	1.2	193	2	AE1561	weakly molybdopter
302	6	1.2	162	2	T17036	NADH2 dehydrogenas	375	6	1.2	193	2	AF1204	molybdopterin-guan
303	6	1.2	162	2	T14247	NADH2 dehydrogenas	376	6	1.2	194	2	C82041	general secretion
304	6	1.2	162	2	T17035	NADH2 dehydrogenas	377	6	1.2	194	2	T45625	hypothetical prote
305	6	1.2	162	2	T17041	NADH2 dehydrogenas	378	6	1.2	196	2	AD0004	conserved hypothet
306	6	1.2	162	2	T14250	NADH2 dehydrogenas	379	6	1.2	196	2	T01954	hypothetical prote
307	6	1.2	162	2	T14248	NADH2 dehydrogenas	380	6	1.2	196	2	E90273	conserved hypothet
308	6	1.2	162	2	T14251	NADH2 dehydrogenas	381	6	1.2	196	2	G65039	hypothetical prote
309	6	1.2	162	2	T17040	NADH2 dehydrogenas	382	6	1.2	196	2	E72610	hypothetical prote
310	6	1.2	162	2	T14249	NADH2 dehydrogenas	383	6	1.2	197	2	S21388	type I keratin 48k
311	6	1.2	162	2	T17042	NADH2 dehydrogenas	384	6	1.2	198	2	C28544	methyl coenzyme M
312	6	1.2	162	2	T14257	NADH2 dehydrogenas	385	6	1.2	198	2	D69022	conserved hypothet
313	6	1.2	162	2	T14252	NADH2 dehydrogenas	386	6	1.2	198	2	A75324	hypothetical prote
314	6	1.2	162	2	T17037	NADH2 dehydrogenas	387	6	1.2	198	2	S60923	hypothetical prote
315	6	1.2	162	2	T17034	NADH2 dehydrogenas	388	6	1.2	198	2	E71837	protein-export mem
316	6	1.2	162	2	T17038	NADH2 dehydrogenas	389	6	1.2	199	2	A48513	macrophage 23K str
317	6	1.2	162	2	T17043	NADH2 dehydrogenas	390	6	1.2	199	2	I52425	probable thioredox
318	6	1.2	162	2	T17039	NADH2 dehydrogenas	391	6	1.2	199	2	AF0947	probable haloacid
319	6	1.2	162	2	T14254	NADH2 dehydrogenas	392	6	1.2	199	2	B95234	DNA-binding respon
320	6	1.2	162	2	T14253	NADH2 dehydrogenas	393	6	1.2	199	2	D98098	response regulator
321	6	1.2	162	2	T14255	NADH2 dehydrogenas	394	6	1.2	199	2	E96926	uracyl DNA glycosi

395	6	1.2	199	2	H90024	hypothetical prote	468	1.2	227	2	C69432	hypothetical prote
396	6	1.2	199	2	AF1303	conserved hypothet	469	1.2	228	2	S05439	dnak-type molecula
397	6	1.2	199	2	AF1675	conserved hypothet	470	1.2	228	2	E87612	cytochrome c, memb
398	6	1.2	200	2	I51016	proliferation asso	471	1.2	229	2	A61133	prolactin precuso
399	6	1.2	200	2	D64405	methyl coenzyme M	472	1.2	229	2	A60972	SSU ribosomal prot
400	6	1.2	200	2	E89871	hypothetical prote	473	1.2	229	2	F69489	glycine betaine/ca
401	6	1.2	201	2	G64676	protein translocat	474	1.2	229	2	F69670	ribosomal protein
402	6	1.2	202	2	G71295	conserved hypothet	475	1.2	230	2	S25964	probable permease
403	6	1.2	203	2	S50980	NHP10 protein - ye	476	1.2	230	2	H83001	conserved hypothet
404	6	1.2	203	2	T52222	hypothetical prote	477	1.2	231	2	F70471	hypothetical prote
405	6	1.2	204	2	T33362	hypothetical prote	478	1.2	231	2	S74286	probable permease
406	6	1.2	204	2	T07423	actin - Chlorella	479	1.2	232	2	H83122	probable ABC trans
407	6	1.2	205	2	B82754	conserved hypothet	480	1.2	232	2	C95294	hypothetical prote
408	6	1.2	205	2	F83075	peptidyl-prolyl ci	481	1.2	232	2	T21359	hypothetical prote
409	6	1.2	205	2	H91229	probable phosphata	482	1.2	232	2	A84732	hypothetical prote
410	6	1.2	206	2	G86076	probable phosphata	483	1.2	233	2	C64429	hypothetical prote
411	6	1.2	206	2	S40829	hypothetical 23.5K	484	1.2	234	2	F82213	DNA-binding respon
412	6	1.2	206	2	S15205	superoxide dismuta	485	1.2	234	2	B69975	probable beta-keto
413	6	1.2	207	2	T34644	probable membrane	486	1.2	235	2	A75501	probable beta-keto
414	6	1.2	207	2	S54128	hypothetical 21.4K	487	1.2	235	2	E72805	gp48 protein - Myc
415	6	1.2	208	1	C69093	conserved hypothet	488	1.2	236	2	D86778	acetolactate decar
416	6	1.2	208	2	B44261	dnak-type molecula	489	1.2	237	2	T15702	hypothetical prote
417	6	1.2	208	2	T16953	hypothetical prote	490	1.2	237	2	H84732	hypothetical prote
418	6	1.2	209	2	C44261	dnak-type molecula	491	1.2	238	1	DECSI	succinate dehydrog
419	6	1.2	209	2	A44261	dnak-type molecula	492	1.2	238	2	E90722	succinate dehydrog
420	6	1.2	209	2	D96755	hypothetical prote	493	1.2	238	2	D85573	succinate dehydrog
421	6	1.2	209	2	H85644	hypothetical prote	494	1.2	238	2	T11718	hypothetical prote
422	6	1.2	209	2	C90785	probable anti-repr	495	1.2	238	2	D85573	hypothetical prote
423	6	1.2	209	2	S76973	hypothetical prote	496	1.2	238	2	T24314	hypothetical prote
424	6	1.2	210	2	A83097	probable glutathio	497	1.2	239	2	S54837	hypothetical prote
425	6	1.2	211	2	AE0552	probable outer mem	498	1.2	240	2	B75187	1-(5-phosphoribos
426	6	1.2	212	2	E87712	amidotransferase H	499	1.2	240	2	G72295	pyruvate formate-1
427	6	1.2	213	2	T33352	hypothetical prote	500	1.2	240	2	T33698	hypothetical prote
428	6	1.2	214	2	B72658	hypothetical prote	501	1.2	240	2	AD0534	conserved hypothet
429	6	1.2	214	2	S78307	plastoquinol-plast	502	1.2	241	2	T27262	hypothetical prote
430	6	1.2	215	2	I40299	variable outer mem	503	1.2	241	2	B87337	hypothetical prote
431	6	1.2	215	2	I64004	hypothetical prote	504	1.2	243	2	S30993	gene 48 protein -
432	6	1.2	216	2	AB1052	probable hexulose-	505	1.2	243	2	D82583	hypothetical prote
433	6	1.2	217	2	T26669	hypothetical prote	506	1.2	244	2	B95166	ABC transporter, A
434	6	1.2	217	2	E82609	conserved hypothet	507	1.2	244	2	G69299	hypothetical prote
435	6	1.2	218	1	Q0EC24	probable transcrip	508	1.2	244	2	T20349	hypothetical prote
436	6	1.2	218	2	D90960	probable 2-compone	509	1.2	244	2	T01761	hypothetical prote
437	6	1.2	218	2	E85808	probable 2-compone	510	1.2	245	2	A30154	IgE receptor alpha
438	6	1.2	218	2	AE0749	invasion response-	511	1.2	245	2	E95943	probable choline u
439	6	1.2	218	2	AE2765	hypothetical prote	512	1.2	245	2	B83108	hypothetical prote
440	6	1.2	219	2	B41886	flagellar membrane	513	1.2	245	2	B90261	glutaconate CoA-tr
441	6	1.2	221	2	F98146	probable amino-aci	514	1.2	245	2	T51081	hypothetical prote
442	6	1.2	221	2	AF3141	hypothetical prote	515	1.2	246	2	A38678	mast cell proteina
443	6	1.2	222	2	S10728	calcium channel pr	516	1.2	246	2	T25532	hypothetical prote
444	6	1.2	222	2	H70920	hypothetical prote	517	1.2	247	2	S45113	granzyme-like prot
445	6	1.2	222	2	D69034	conserved hypothet	518	1.2	247	2	A25773	dnak-type molecula
446	6	1.2	223	2	AG1615	betaine/carnitine/	519	1.2	247	2	D91066	hypothetical membr
447	6	1.2	223	2	A11252	betaine/carnitine/	520	1.2	248	2	AD1218	cobalamin (5'-phos
448	6	1.2	223	2	D84297	hypothetical prote	521	1.2	248	2	F72262	ubiquinone/menaqui
449	6	1.2	224	2	T20584	hypothetical prote	522	1.2	249	2	T03011	dnac protein homol
450	6	1.2	224	2	G72746	branched-chain ami	523	1.2	249	2	AG0618	probable DNA repli
451	6	1.2	224	2	B69277	hypothetical prote	524	1.2	249	2	E72646	probable molybdopt
452	6	1.2	224	2	D95335	hypothetical prote	525	1.2	250	2	H97448	hemolysin importe
453	6	1.2	225	2	AH0839	probable transcrip	526	1.2	250	2	AB2667	hemolysin importe
454	6	1.2	226	2	B69670	choline ABC transp	527	1.2	251	1	HVCY	astacin EC 3.4.24
455	6	1.2	226	2	A84969	hypothetical prote	528	1.2	251	2	I57668	luteinizing hormon
456	6	1.2	226	2	T24056	hypothetical prote	529	1.2	252	2	T13588	NADH2 dehydrogenas
457	6	1.2	226	2	G75342	hypothetical prote	530	1.2	252	2	D85910	unknown protein en
458	6	1.2	226	2	T17328	hypothetical prote	531	1.2	252	2	B83801	ABC transporter (p
459	6	1.2	226	2	C72102	ct179 hypothetical	532	1.2	253	2	H83417	hypothetical prote
460	6	1.2	226	2	F86519	hypothetical prote	533	1.2	254	2	S01100	hemolymph 30K prot
461	6	1.2	226	2	A87664	hypothetical prote	534	1.2	254	2	AC2163	hypothetical prote
462	6	1.2	226	2	T35435	probable integral	535	1.2	254	2	S35008	modulation protein
463	6	1.2	227	2	T44913	probable serine o-	536	1.2	254	2	D83446	hypothetical prote
464	6	1.2	227	2	S77870	dnak-type molecula	537	1.2	254	2	T40100	conserved phosduc
465	6	1.2	227	2	B71358	hypothetical prote	538	1.2	255	2	A70758	hypothetical prote
466	6	1.2	227	2	T42015	probable RNA polym	539	1.2	255	2	T48543	hypothetical prote
467	6	1.2	227	2			540	1.2	255	2	AF0515	DedA family integr

541	6	1.2	256	2	S17662	hemolymph 30K prot	614	6	1.2	279	2	D84185	hypothetical prote
542	6	1.2	256	2	S23691	erythrocyte membra	615	6	1.2	279	2	H87917	protein F28D9.1 [i
543	6	1.2	256	2	J01144	H+-transporting tw	616	6	1.2	279	2	D90258	hypothetical prote
544	6	1.2	256	2	A35340	H+-transporting tw	617	6	1.2	280	2	C70696	probable transport
545	6	1.2	257	2	A83190	3-oxoacyl-(acyl-ca	618	6	1.2	280	2	AE2026	hypothetical prote
546	6	1.2	257	2	I37532	MHC class II histo	619	6	1.2	281	2	AD3369	universal stress p
547	6	1.2	258	2	A75618	probable chromosom	620	6	1.2	282	2	AF0902	dihydropteroate sy
548	6	1.2	259	2	H83920	transcription regu	621	6	1.2	282	2	D72771	probable bacterio
549	6	1.2	259	2	D97613	hypothetical prote	622	6	1.2	282	2	T20402	hypothetical prote
550	6	1.2	259	2	A12835	N-acetylmuramoyl-L	623	6	1.2	282	2	AF1530	conserved hypothet
551	6	1.2	260	2	D82366	ubiquinone/menaqui	624	6	1.2	283	2	T33705	hypothetical prote
552	6	1.2	260	2	A57245	VAMP-binding prote	625	6	1.2	283	2	T51091	hypothetical prote
553	6	1.2	261	2	S17886	MHC class II histo	626	6	1.2	283	2	G84457	probable mufc doma
554	6	1.2	261	2	I37531	MHC class II histo	627	6	1.2	283	2	JC5661	hepatoma-derived g
555	6	1.2	261	2	JC4110	triacylglycerol li	628	6	1.2	285	2	F83890	sugar transport sy
556	6	1.2	261	2	D96029	probable CoA-trans	629	6	1.2	285	2	B84316	halocyanin precurs
557	6	1.2	261	2	A65029	rhodanese-like pro	630	6	1.2	285	2	T29832	hypothetical prote
558	6	1.2	261	2	D91052	enhanced serine se	631	6	1.2	286	2	S73423	spermidine/putresc
559	6	1.2	261	2	AF0823	SseB protein limpo	632	6	1.2	286	2	JE0417	aminoglycoside-N-a
560	6	1.2	261	2	S63604	hemeobox protein-G	633	6	1.2	286	2	T26657	hypothetical prote
561	6	1.2	261	2	A99421	hypothetical prote	634	6	1.2	286	2	G75437	conserved hypothet
562	6	1.2	261	2	B95273	hypothetical prote	635	6	1.2	287	2	S57770	xyloglucan endo-1,
563	6	1.2	262	2	F82959	permease of ABC zi	636	6	1.2	288	2	B71470	probable kinase -
564	6	1.2	262	2	T34115	hypothetical prote	637	6	1.2	288	2	T04401	endonuclease (EC 3
565	6	1.2	263	2	S44668	ZK370.7 protein -	638	6	1.2	288	2	C83518	hypothetical prote
566	6	1.2	264	2	C64701	hypothetical prote	639	6	1.2	288	2	B43253	zinc finger protei
567	6	1.2	264	2	G90339	conserved hypothet	640	6	1.2	289	2	S68445	probable glucosami
568	6	1.2	264	2	D69811	hypothetical prote	641	6	1.2	289	2	S49812	xyloglucan endo-1,
569	6	1.2	264	2	T16271	hypothetical prote	642	6	1.2	289	2	A34783	myogenesis protein
570	6	1.2	265	2	E64128	lic-1 protein D -	643	6	1.2	290	2	D97459	sulfate transport
571	6	1.2	265	2	A10437	hypothetical prote	644	6	1.2	290	2	AF2677	ABC transporter, m
572	6	1.2	265	2	T34755	hypothetical prote	645	6	1.2	290	2	S36706	B4 protein - equin
573	6	1.2	266	2	D87265	hypothetical prote	646	6	1.2	290	2	G71623	rifin PFB0065w - m
574	6	1.2	266	2	S67436	hypothetical prote	647	6	1.2	290	2	AG2309	hypothetical prote
575	6	1.2	266	2	S40988	hypothetical prote	648	6	1.2	290	2	A12460	hypothetical prote
576	6	1.2	266	2	B84848	hypothetical prote	649	6	1.2	291	2	A98325	dipeptide ABC tran
577	6	1.2	268	2	G70553	probable echal0 pr	650	6	1.2	291	2	AE2958	hypothetical prote
578	6	1.2	268	2	D33465	lic-1 protein D -	651	6	1.2	291	2	D96002	probable sugar upt
579	6	1.2	269	2	S32427	triase-phosphate i	652	6	1.2	291	2	E82880	translation elonga
580	6	1.2	269	2	AG3638	inositol-1(or 4)-m	653	6	1.2	291	2	A70512	probable preB prot
581	6	1.2	269	2	A83086	conserved hypothet	654	6	1.2	292	2	S76003	hypothetical prote
582	6	1.2	269	2	T44866	hypothetical prote	655	6	1.2	292	2	T45680	hypothetical prote
583	6	1.2	269	2	H85896	enhanced serine se	656	6	1.2	292	2	D97199	probable membrane
584	6	1.2	269	2	T36910	hypothetical prote	657	6	1.2	292	2	H96784	hypothetical prote
585	6	1.2	269	2	T08811	hypothetical prote	658	6	1.2	292	2	D71181	hypothetical prote
586	6	1.2	269	2	A96995	cobalt permease [i	659	6	1.2	292	2	AG3524	high-affinity bran
587	6	1.2	270	2	AF1172	mannose-specific p	660	6	1.2	293	2	H82184	glycerol-3-phospha
588	6	1.2	270	2	B75325	hypothetical prote	661	6	1.2	293	2	I39620	hypothetical prote
589	6	1.2	270	2	AD3634	noro protein limpo	662	6	1.2	295	1	QOSABT	hypothetical prote
590	6	1.2	271	2	E70240	pfs protein (pfs)	663	6	1.2	295	2	AI1291	transcription acti
591	6	1.2	272	2	A69961	geranyltransnstranf	664	6	1.2	295	2	AI1133	hypothetical prote
592	6	1.2	272	2	S27820	vitelline B2 precu	665	6	1.2	295	2	S67934	branched-chain ket
593	6	1.2	272	2	H71124	hypothetical prote	666	6	1.2	296	2	A95962	probable SDR fami
594	6	1.2	273	2	G87347	flagellin FljO [im	667	6	1.2	297	2	AB3037	hypothetical prote
595	6	1.2	273	2	E70572	hypothetical prote	668	6	1.2	297	2	E84733	nicotinate-nucleot
596	6	1.2	274	2	G83186	hypothetical prote	669	6	1.2	297	2	A99643	quinolinate phosph
597	6	1.2	275	2	E91102	probable enzyme [i	670	6	1.2	297	2	A85494	quinolinate phosph
598	6	1.2	275	2	A85948	probable enzyme yg	671	6	1.2	297	2	JL0032	hypothetical prote
599	6	1.2	275	2	F65076	hypothetical prote	672	6	1.2	297	2	C82787	hypothetical prote
600	6	1.2	275	2	H82565	conserved hypothet	673	6	1.2	298	2	AB7147	methyl mycolic aci
601	6	1.2	275	2	S40903	FUN4 protein - yea	674	6	1.2	298	2	G72531	hypothetical prote
602	6	1.2	275	2	D97525	hypothetical prote	675	6	1.2	299	2	A70948	probable hpx prote
603	6	1.2	276	2	T12552	hypothetical prote	676	6	1.2	299	2	A98249	nitrate transport
604	6	1.2	276	2	H86922	probable ABC trans	677	6	1.2	300	2	S60164	transcription init
605	6	1.2	276	2	D87407	conserved hypothet	678	6	1.2	300	2	E97653	RNA polymerase sig
606	6	1.2	276	2	H75588	conserved hypothet	679	6	1.2	300	2	AC2877	RNA polymerase sig
607	6	1.2	277	2	AG3534	oligopeptide trans	680	6	1.2	300	2	G95954	probable dUDP-4-de
608	6	1.2	278	2	I51344	dnak-type molecula	681	6	1.2	301	1	R0RBT5	cytochrome-b5 redu
609	6	1.2	278	2	T19813	hypothetical prote	682	6	1.2	301	2	E72289	oligopeptide ABC t
610	6	1.2	278	2	C95281	hypothetical prote	683	6	1.2	301	2	G72613	probable mmaM4 pro
611	6	1.2	278	2	B81384	hypothetical prote	684	6	1.2	302	2	C72756	probable multiple
612	6	1.2	279	2	E81951	probable transmemb	685	6	1.2	302	2	AB0416	nicotinate-nucleot
613	6	1.2	279	2	B70115	translation elonga	686	6	1.2	302	2	T34398	hypothetical prote

687	6	1.2	302	2	F95990	probable transcript	760	6	1.2	323	2	T51621	myb-like protein f
688	6	1.2	302	2	S77382	hypothetical prote	761	6	1.2	323	2	T51645	myb-related transc
689	6	1.2	302	2	D70538	probable bpoB prot	762	6	1.2	323	2	T45531	agaB protein [impo
690	6	1.2	304	2	C82760	UDP-3-O-[3-hydroxy	763	6	1.2	323	2	S73189	prenyl transferase
691	6	1.2	304	2	T42554	tegument protein -	764	6	1.2	323	2	H70765	hypothetical prote
692	6	1.2	304	2	T45469	cell wall lipoprot	765	6	1.2	324	2	A83584	conserved hypothet
693	6	1.2	304	2	T10212	hypothetical prote	766	6	1.2	325	2	C89844	hypothetical prote
694	6	1.2	305	2	JC5361	deoxyribonuclease	767	6	1.2	326	1	QRECB	vitamin B12 transp
695	6	1.2	305	2	B87499	oxidoreductase, Gf	768	6	1.2	326	2	AC0705	vitamin B12 transp
696	6	1.2	307	2	AE0432	conserved hypothet	769	6	1.2	326	2	F85779	vitamin B12 transp
697	6	1.2	307	2	A20852	catechol 2,3-dioxy	770	6	1.2	326	2	B90931	vitamin B12 transp
698	6	1.2	307	2	S47421	catechol 2,3-dioxy	771	6	1.2	326	2	H72472	hypothetical prote
699	6	1.2	307	2	JC5654	catechol 2,3-dioxy	772	6	1.2	326	2	C71426	hypothetical prote
700	6	1.2	307	2	G90195	conserved hypothet	773	6	1.2	326	2	S61517	fibulin-1 precurs
701	6	1.2	307	4	S58112	catechol 2,3-dioxy	774	6	1.2	327	1	S45529	NADPH2:quinone red
702	6	1.2	308	2	AE0432	ferric anguibactin	775	6	1.2	327	2	A98258	quinone oxidoreduc
703	6	1.2	308	2	S74719	hypothetical prote	776	6	1.2	327	2	B66098	quinone oxidoreduc
704	6	1.2	308	2	C89866	oligopeptide trans	777	6	1.2	327	2	JC5319	macrolide-lincosam
705	6	1.2	310	2	A24999	L-lactate dehydrog	778	6	1.2	327	2	E72120	transaldolase - Ch
706	6	1.2	310	2	AB3329	tRNA isopentenyltr	779	6	1.2	327	2	C86501	chain length deter
707	6	1.2	310	2	S67181	hypothetical prote	780	6	1.2	327	2	S33672	polysaccharide cha
708	6	1.2	310	2	S58090	probable membrane	781	6	1.2	327	2	AC0765	conserved hypothet
709	6	1.2	312	2	B70826	probable echA4 pro	782	6	1.2	327	2	AG0062	hypothetical prote
710	6	1.2	312	2	A83486	cobalamin biosynth	783	6	1.2	327	2	S57121	estradiol 17beta-d
711	6	1.2	312	2	A25455	licheninase (EC 3.	784	6	1.2	328	1	DEHUE7	hypothetical prote
712	6	1.2	312	2	AG1302	methionyl-tRNA for	785	6	1.2	328	2	S67570	hypothetical prote
713	6	1.2	312	2	AG1674	transcription regu	786	6	1.2	329	2	S08499	type II DNA modifi
714	6	1.2	312	2	F87615	3-hydroxyisobutyla	787	6	1.2	329	2	H71844	transaldolase CP06
715	6	1.2	313	2	H98227	2-HYDROXY-3-OXOP	788	6	1.2	329	2	D81550	hypothetical prote
716	6	1.2	313	2	AB3058	hypothetical prote	789	6	1.2	329	2	D86733	licheninase (EC 3.
717	6	1.2	313	2	S75329	hypothetical prote	790	6	1.2	329	2	S13735	probable cadmium-t
718	6	1.2	314	2	F98231	succinoglycan bios	791	6	1.2	329	2	T05728	ferrichrome ABC tr
719	6	1.2	314	2	AG3054	succinoglycan bios	792	6	1.2	329	2	AC1718	ribosomal protein
720	6	1.2	314	2	T48514	hypothetical prote	793	6	1.2	329	2	AG1347	tryptophanyl-tRNA
721	6	1.2	314	2	AF6621	hypothetical prote	794	6	1.2	330	1	T43816	rlx protein - Stap
722	6	1.2	315	2	T06053	probable ubiquitin	795	6	1.2	330	2	H75505	tRNA isopentenyl t
723	6	1.2	315	2	D83426	hypothetical prote	796	6	1.2	330	2	S28102	hypothetical prote
724	6	1.2	315	2	T15165	hypothetical prote	797	6	1.2	330	2	T48100	cobalamin biosynth
725	6	1.2	315	2	AD2298	hypothetical prote	798	6	1.2	331	2	E86638	hypothetical prote
726	6	1.2	316	2	B83658	phosphoribosyl pyr	799	6	1.2	331	2	B83486	hypothetical prote
727	6	1.2	316	2	C82085	conserved hypothet	800	6	1.2	331	2	H98020	casein kinase II (
728	6	1.2	316	2	AC1965	proline iminopepti	801	6	1.2	332	2	S19726	probable sugar upt
729	6	1.2	316	2	T44749	hypothetical prote	802	6	1.2	332	2	D95973	TerC family protei
730	6	1.2	316	2	G98184	oligopeptide ABC t	803	6	1.2	332	2	H87705	probable ABC trans
731	6	1.2	316	2	AC3102	hypothetical prote	804	6	1.2	333	2	AI0050	flagellar P-ring p
732	6	1.2	317	2	T18695	hypothetical prote	805	6	1.2	333	2	T37871	hypothetical nucle
733	6	1.2	317	2	S18299	exoz protein - Rhi	806	6	1.2	333	2	F90243	conserved hypothet
734	6	1.2	317	2	E69195	conserved hypothet	807	6	1.2	334	2	S13734	licheninase (EC 3.
735	6	1.2	317	2	T16710	hypothetical prote	808	6	1.2	334	2	S36235	licheninase (EC 3.
736	6	1.2	317	2	B95975	acetyltransferase	809	6	1.2	334	2	T19955	hypothetical prote
737	6	1.2	317	2	A95282	ABC transporter, p	810	6	1.2	334	2	T46238	hypothetical prote
738	6	1.2	318	1	D57987	nrfb protein - Esc	811	6	1.2	334	2	A83414	probable transcript
739	6	1.2	318	2	G91260	formate-dependent	812	6	1.2	335	2	D84321	50S ribosomal prot
740	6	1.2	318	2	C86101	cytochrome c-type	813	6	1.2	335	2	F72404	flagellar motor sw
741	6	1.2	318	2	AG1020	BRO-c - Bombyx mor	814	6	1.2	335	2	T41426	hypothetical wtfs
742	6	1.2	318	2	T41838	succinate dehydrog	815	6	1.2	335	2	T21503	hypothetical prote
743	6	1.2	318	2	E84360	glycosyl transfera	816	6	1.2	335	2	B87590	hypothetical prote
744	6	1.2	318	2	D87506	fiber protein - hu	817	6	1.2	336	2	D716330	hypothetical prote
745	6	1.2	319	1	ERADF3	probable transport	818	6	1.2	336	2	D171474	probable muramoyl-
746	6	1.2	319	2	T37130	membrane-bound com	819	6	1.2	336	2	G46289	flavoprotein (fpra
747	6	1.2	319	2	A87171	hypothetical prote	820	6	1.2	336	2	G69270	hypothetical prote
748	6	1.2	319	2	H69964	hypothetical prote	821	6	1.2	336	2	T20586	hypothetical prote
749	6	1.2	319	2	C72553	probable transcript	822	6	1.2	336	2	T25002	probable ABC-type
750	6	1.2	319	2	F97626	transcription regu	823	6	1.2	337	2	D64896	hypothetical prote
751	6	1.2	319	2	AH2849	probable D-amino a	824	6	1.2	337	2	B85734	hypothetical prote
752	6	1.2	320	2	T32655	hypothetical prote	825	6	1.2	337	2	E90884	hypothetical prote
753	6	1.2	320	2	T03899	hypothetical prote	826	6	1.2	337	2	T36307	hypothetical prote
754	6	1.2	320	2	A13234	hypothetical prote	827	6	1.2	338	2	A56274	sulfur-regulated 3
755	6	1.2	321	2	T25004	hypothetical prote	828	6	1.2	339	2	T28686	hypothetical prote
756	6	1.2	321	2	D81018	iron(III) ABC tran	829	6	1.2	340	2	AF1319	ferrichrome ABC tr
757	6	1.2	321	2	E81962	probable membrane	830	6	1.2	341	2	AF1691	probable sugar upt
758	6	1.2	322	2	C83075	octaprenyl-diphosp	831	6	1.2	341	2	B95970	
759	6	1.2	323	2	A34284	NADH2 dehydrogenas	832	6	1.2	341	2		

833	6	1.2	341	2	B98338	hypothetical 36.0K	906	6	1.2	357	2	S35318	MET22 protein - ye
834	6	1.2	341	2	AH2944	hypothetical prote	907	6	1.2	357	2	C42087	a2-phormone recep
835	6	1.2	341	2	CB3578	hypothetical prote	908	6	1.2	358	1	T03917	GMP reductase (EC
836	6	1.2	341	2	B83298	conserved hypotet	909	6	1.2	358	2	T36415	probable iron-side
837	6	1.2	342	2	T51957	metalloproteinase	910	6	1.2	358	2	B82989	alginate biosynthe
838	6	1.2	342	2	AE0155	probable ABC trans	911	6	1.2	358	2	B83808	hypothetical prote
839	6	1.2	342	2	G84885	probable metallopr	912	6	1.2	358	2	F98289	lps biosynthesis r
840	6	1.2	342	2	T44043	hypothetical prote	913	6	1.2	359	1	OKKWC1	protein kinase (EC
841	6	1.2	342	2	T44229	hypothetical prote	914	6	1.2	359	2	T21211	hypothetical prote
842	6	1.2	342	2	T29115	hypothetical prote	915	6	1.2	359	2	A57718	pheromone receptor
843	6	1.2	342	2	I77461	luteinizing hormon	916	6	1.2	359	2	B59105	hypothetical prote
844	6	1.2	342	2	A98309	iron(III) ABC tran	917	6	1.2	360	2	H82081	phospho-N-acetylmu
845	6	1.2	342	2	AE2974	hypothetical prote	918	6	1.2	360	2	B83063	peptide chain rele
846	6	1.2	343	2	D71509	probable proteinas	919	6	1.2	360	2	S36750	cannabinoid recept
847	6	1.2	343	2	E95971	probable exported	920	6	1.2	360	2	G90269	transposase ISC125
848	6	1.2	343	2	AH3159	replication protei	921	6	1.2	360	2	C84243	asparagine synthet
849	6	1.2	344	2	T17056	NADH2 dehydrogenas	922	6	1.2	360	2	S09552	nodulin - soybean
850	6	1.2	344	2	H86503	cytochrome oxidase	923	6	1.2	360	2	JE0116	zinc-finger protei
851	6	1.2	344	2	G72119	cytochrome D ubiqu	924	6	1.2	361	2	B84716	hypothetical prote
852	6	1.2	344	2	C97381	glucokinase (gluco	925	6	1.2	361	2	T42517	bromodomain protei
853	6	1.2	344	2	AB2599	glucokinase [impor	926	6	1.2	362	1	F64302	cobalamin biosynth
854	6	1.2	344	2	T01629	probable GDSL-moti	927	6	1.2	362	2	S17285	hypothetical prote
855	6	1.2	344	2	D84450	hypothetical prote	928	6	1.2	362	2	A71269	conserved hypotet
856	6	1.2	345	2	T7062	NADH2 dehydrogenas	929	6	1.2	363	2	A31342	fructose-bisphosph
857	6	1.2	345	2	T34031	hypothetical prote	930	6	1.2	363	2	T10638	probable riboflavi
858	6	1.2	345	2	T29264	hypothetical prote	931	6	1.2	363	2	T27335	hypothetical prote
859	6	1.2	345	2	T29243	hypothetical prote	932	6	1.2	364	2	E82159	probable periplasm
860	6	1.2	346	2	C98830	glucanase homolog	933	6	1.2	365	2	E87004	conserved hypotet
861	6	1.2	346	2	D72705	hypothetical prote	934	6	1.2	365	2	A84056	hypothetical prote
862	6	1.2	346	2	T09927	cytidine deaminase	935	6	1.2	365	2	H98217	nspC protein (AE00
863	6	1.2	346	2	T19676	hypothetical prote	936	6	1.2	365	2	AC3069	carboxynorspermid
864	6	1.2	346	2	AG1144	conserved hypotet	937	6	1.2	365	2	AG3450	carboxynorspermid
865	6	1.2	346	2	AG1503	conserved hypotet	938	6	1.2	366	1	D70351	probable hexosyltr
866	6	1.2	346	2	T24516	hypothetical prote	939	6	1.2	366	1	SZB55E	stage V sporulatio
867	6	1.2	347	2	E81154	heat shock protein	940	6	1.2	367	2	T35929	probable alcohol d
868	6	1.2	347	2	S70364	cannabinoid recept	941	6	1.2	367	2	T33119	hypothetical prote
869	6	1.2	347	2	G96741	unknown protein F1	942	6	1.2	367	2	JE0349	interferon-inducib
870	6	1.2	347	2	T06671	hypothetical prote	943	6	1.2	367	2	S69586	hypothetical prote
871	6	1.2	347	2	A12310	hypothetical prote	944	6	1.2	367	2	A83681	ABC transporter (p
872	6	1.2	348	2	I50107	MHC class I histoc	945	6	1.2	368	1	QOBEF4	gene 59 protein -
873	6	1.2	349	2	B83434	translocation prot	946	6	1.2	368	2	C70786	probable liveE prot
874	6	1.2	349	2	A00990	probable membrane	947	6	1.2	368	2	T44887	probable branched-
875	6	1.2	349	2	B99420	hypothetical prote	948	6	1.2	369	2	B84356	AAA-type AtPase [1
876	6	1.2	350	2	AD1555	glucanase and pept	949	6	1.2	370	2	AB2118	UDP-N-acetyl gluc
877	6	1.2	350	2	AF1197	glucanase and pept	950	6	1.2	371	2	D75266	cell division prot
878	6	1.2	350	2	T33798	hypothetical prote	951	6	1.2	371	2	S76682	hypothetical prote
879	6	1.2	350	2	T05589	hypothetical prote	952	6	1.2	374	2	T29154	hypothetical prote
880	6	1.2	350	2	F99883	cell surface prote	953	6	1.2	374	2	B81324	probable ubiquinol
881	6	1.2	350	2	AE3171	ATP-dependent DNA	954	6	1.2	375	1	OKKWC2	protein kinase (EC
882	6	1.2	351	2	D84788	hypothetical prote	955	6	1.2	375	2	T21212	hypothetical prote
883	6	1.2	351	2	S56172	translation initia	956	6	1.2	375	2	D96037	probable ABC trans
884	6	1.2	352	2	S19027	protein kinase A (957	6	1.2	375	2	JN0618	Gal beta 1,3(4)Glc
885	6	1.2	352	2	T39363	RNA binding protei	958	6	1.2	376	2	AE1786	cell division prot
886	6	1.2	353	1	JQ1946	core protein VP7 -	959	6	1.2	376	2	C95878	probable dehydrog
887	6	1.2	353	2	E83577	D-erythrose 4-phos	960	6	1.2	376	2	G84404	hypothetical prote
888	6	1.2	353	2	C31751	protein kinase (EC	961	6	1.2	377	2	C39827	4-coumarate-CoA li
889	6	1.2	353	2	B83848	ferric ion ABC tra	962	6	1.2	377	2	S64687	morphinone reducta
890	6	1.2	353	2	S65086	finger protein XFO	963	6	1.2	377	2	T47791	hypothetical prote
891	6	1.2	353	2	C72479	hypothetical prote	964	6	1.2	377	2	A47380	RING finger-contai
892	6	1.2	354	2	H95011	glycosyl transfera	965	6	1.2	377	2	H89717	protein C18B12.2 l
893	6	1.2	354	2	AB3537	oligopeptide trans	966	6	1.2	378	2	S14959	proline-rich prote
894	6	1.2	355	2	T07160	glutamate-ammonia	967	6	1.2	378	2	JC5245	G protein-coupled
895	6	1.2	356	1	AJAAQ	glutamate-ammonia	968	6	1.2	378	2	C83465	flagellar biosynth
896	6	1.2	356	1	AJFBOB	glutamate-ammonia	969	6	1.2	378	2	B71156	hypothetical prote
897	6	1.2	356	1	AJFBOQ	glutamate-ammonia	970	6	1.2	379	1	A56685	UDPglucose-hexose
898	6	1.2	356	2	T71579	glutamate-ammonia	971	6	1.2	379	2	S58452	ubiquinol-cytochro
899	6	1.2	356	2	E84199	hypothetical prote	972	6	1.2	379	2	T11414	ubiquinol-cytochro
900	6	1.2	356	2	B95999	probable iron ABC	973	6	1.2	379	2	A44473	UTP-hexose-1-phosp
901	6	1.2	357	1	QOBE14	BMRF2 protein - hu	974	6	1.2	379	2	I57459	galactose-1-phosph
902	6	1.2	357	2	S36195	glutamate-ammonia	975	6	1.2	379	2	G97265	probable cysteine
903	6	1.2	357	2	F84304	cell division prot	976	6	1.2	379	2	AB2423	hypothetical prote
904	6	1.2	357	2	H98819	conserved hypotet	977	6	1.2	379	2	F91271	hypothetical prote
905	6	1.2	357	2	G75552	riboflavin bifunct	978	6	1.2	379	2	G75170	hypothetical prote

979 6 1.2 379 2 F86112 hypothetical prote
980 6 1.2 380 2 T13758 NADH2 dehydrogenas
981 6 1.2 380 2 T46395 hypothetical prote
982 6 1.2 381 2 T31137 multidrug resistanc
983 6 1.2 381 2 C96657 hypothetical prote
984 6 1.2 381 2 T09640 protein phosphatas
985 6 1.2 381 2 T34015 hypothetical prote
986 6 1.2 382 2 D96922 uncharacterized me
987 6 1.2 383 1 VGBEKG glycoprotein precu
988 6 1.2 383 2 T12656 NADH2 dehydrogenas
989 6 1.2 383 2 S53716 delta-like homeoti
990 6 1.2 383 2 B96607 hypothetical prote
991 6 1.2 384 1 BVECCX membrane protein c
992 6 1.2 384 2 T61769 keratin 6d, type I
993 6 1.2 384 2 F85528 cyanate transport
994 6 1.2 384 2 B90678 cyanate transport
995 6 1.2 385 1 S29844 transforming prote
996 6 1.2 385 2 A91006 probable transport
997 6 1.2 385 2 B85850 probable transport
998 6 1.2 385 2 C97883 conserved hypothet
999 6 1.2 385 2 A64981 yehy protein - Esc
1000 6 1.2 386 2 A57066 prostacyclin recep

ALIGNMENTS

RESULT 1
E69791
conserved hypothetical protein yebA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
R:Accession: E69791
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69791
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-655 <RUN>
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12454.1; PID:el182614;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yebA

Query Match 1.8%; Score 9; DB 2; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 431 VLAVLLVAA 439
|||||||
Db 565 VLAVLLVAA 573

RESULT 2
T36146
hypothetical protein SCE19_23c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36146

R:Seeger, K.; Harris, D.; Harris, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T36146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-224 <SEE>
A:Cross-references: EMBL:AL096852; PIDN:CAB51004.1; GSPDB:GN00070; SCOEDB:SCE19.23c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE19.23c

Query Match 1.6%; Score 8; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 GIVLAVLL 436
|||||||
Db 132 GIVLAVLL 139

RESULT 3
T30232
methyltransferase homolog - Streptomyces hygroscopicus
C:Species: Streptomyces hygroscopicus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T30232
R:Aparicio, J.F.; Molnar, I.; Schwecke, T.; Koenig, A.; Haydock, S.F.; Khaw, L.E.; St
Gene 169, 9-16, 1996
A:Title: Organization of the biosynthetic gene cluster for rapamycin in Streptomyces
A:Reference number: Z20782; MUID:96186896; PMID:8635756
A:Accession: T30232
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-317 <A>
A:Cross-references: EMBL:X86780; NID:g987088; PID:g987106; PIDN:CAA60466.1
C:Genetics:
A:Gene: rapM

Query Match 1.6%; Score 8; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LREAARAL 19
|||||||
Db 188 LREAARAL 195

RESULT 4
E84280
hypothetical protein Vng1250h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84280
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84280
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: GB:AE004437; NID:gl0580777; PIDN:AAG19609.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG1250H

Query Match 1.6%; Score 8; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 LAVLLVAA 439
 |||||
 Db 17 LAVLLVAA 24

RESULT 5

arisenical pump membrane protein - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C:Accession: C41903
 R:Ji, G.; Silver, S.
 J. Bacteriol. 174, 3684-3694, 1992
 A:Title: Regulation and expression of the arsenic resistance operon from Staphylococcus
 A:Reference number: A41903; MUID:92276351; PMID:1534328
 A:Contents: p1258
 A:Accession: C41903
 A:Molecule type: DNA
 A:Residues: 1-429 <J11>
 A:CROSS-references: GB:M86824; NID:g150725; PIDN:AAA25637.1; PID:g150728
 A:Note: sequence extracted from NCBI backbone (NCBIN:104669, NCBIP:104672)
 C:Genetics:
 A:Gene: arsB
 C:Superfamily: arsenical pump membrane protein
 C:Keywords: toxic oxyanion resistance; transmembrane protein

Query Match 1.6%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 IVLAVLLV 437
 |||||
 Db 230 IVLAVLLV 237

RESULT 6

probable sodium/alanine symporter NMA1901 [imported] - Neisseria meningitidis (strain 22
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: E81817
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
 A:Reference number: A81775; MUID:2022556; PMID:10761919
 A:Accession: E81817
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-472 <PAR>
 A:CROSS-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85122.1; PID:g738053
 A:Experimental source: serogroup A, strain 22491
 C:Genetics:
 A:Gene: NMA1901
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein.

Query Match 1.6%; Score 8; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIVLAVL 435
 |||||
 Db 195 VGIVLAVL 202

RESULT 7

amino acid symporter, probable NMB1647 [imported] - Neisseria meningitidis (strain MC58
 F81058
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: F81058
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: F81058
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-472 <TET>
 A:CROSS-references: GB:AE002515; GB:AE002098; NID:g7226894; PIDN:AAF41996.1; PID:g722
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1647
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 1.6%; Score 8; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIVLAVL 435
 |||||
 Db 195 VGIVLAVL 202

RESULT 8

hypothetical protein C36E8.3 - Caenorhabditis elegans
 T19786
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T19786
 R:Wilkinson, J.; Barlow, K.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: Z19177
 A:Accession: T19786
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-476 <WIL>
 A:CROSS-references: EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C36E8.3
 A:Experimental source: clone C36E8
 C:Genetics:
 A:Gene: CESP:C36E8.3
 A:Map position: 3
 A:Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 1.6%; Score 8; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 TIATGGFI 159
 |||||
 Db 171 TIATGGFI 178

RESULT 9

export protein - Streptomyces coelicolor
 T35715
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C:Accession: T35715
 R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z21548
 A:Accession: T35715
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <MUR>
 A:CROSS-references: EMBL:AL021411; PIDN:CAA16207.1; GSPDB:GN00070; SCOEDB:SC7H1.20c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC7H1.20c
 C:Superfamily: lincomycin-resistance protein lmrB

Query Match 1.6%; Score 8; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 VLAVLLVA 438
 |||||
 DB 29 VLAVLLVA 36

RESULT 10
 AI2507
 hypothetical protein alr7241 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AI2507
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AI2507
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-562 <KUR>
 A:Cross-references: GB:BA000020; PIDN:BA078325.1; PID:g17135779; GSPDB:GN00180
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr7241
 A:Genome: plasmid

Query Match 1.6%; Score 8; DB 2; Length 562;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 SPYDGLT 381
 |||||
 DB 481 SPYDGLT 488

RESULT 11
 T46517
 hypothetical protein gra-orf12 [imported] - Streptomyces violaceoruber
 C:Species: Streptomyces violaceoruber
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 11-May-2000
 C:Accession: T46517
 R:Ichinose, K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; Flos
 Chem. Biol. 5, 647-659, 1998
 A:Title: The granaticin biosynthetic gene cluster of Streptomyces violaceoruber Tu22: se
 A:Reference number: Z23045; MUID:99051446; PMID:9831526
 A:Accession: T46517
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-751 <TCH>
 A:Cross-references: EMBL:AJ011500; PIDN:CAA09633.1
 A:Experimental source: strain Tu22
 C:Genetics:
 A:Note: gra-orf12

Query Match 1.6%; Score 8; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLREAARA 18
 |||||
 DB 38 VLREAARA 45

RESULT 12
 W5WL33
 E5 protein - human papillomavirus type 33
 C:Species: human papillomavirus type 33
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999

C:Accession: A03679
 R:Cole, S.T.; Strebeck, R.E.
 J. Virol. 58, 991-995, 1986
 A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33,
 A:Reference number: A93020; MUID:86200464; PMID:3009902
 A:Accession: A03679
 A:Molecule type: DNA
 A:Residues: 1-75 <COL>
 A:Cross-references: GB:M12732; NID:g333049; PIDN:AAA46962.1; PID:g463181
 C:Superfamily: papillomavirus E5 protein
 C:Keywords: early protein

Query Match 1.4%; Score 7; DB 1; Length 75;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLLVLVL 12
 |||||
 DB 31 WLLVLVL 37

RESULT 13
 W5WL58
 E5 protein - human papillomavirus type 58
 C:Species: human papillomavirus type 58
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
 C:Accession: D36779
 R:Kirii, Y.; Iwamoto, S.; Matsukura, T.
 Virology 185, 424-427, 1991
 A:Title: Human papillomavirus type 58 DNA sequence.
 A:Reference number: A36779; MUID:92024102; PMID:1656594
 A:Accession: D36779
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-76 <KIR>
 A:Cross-references: GB:D90400; NID:g222386; PIDN:BAA31849.1; PID:g3337102
 C:Superfamily: papillomavirus E5 protein
 C:Keywords: early protein

Query Match 1.4%; Score 7; DB 1; Length 76;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLLVLVL 12
 |||||
 DB 32 WLLVLVL 38

RESULT 14
 S08449
 hypothetical protein 9 - spiroplasma virus 1
 C:Species: spiroplasma virus 1, Spv1
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 07-Dec-1999
 C:Accession: S08449
 R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
 Nucleic Acids Res. 18, 1293, 1990
 A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus Spv1-R
 A:Reference number: S08447; MUID:90206799; PMID:2320423
 A:Accession: S08449
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-78 <REN>
 A:Cross-references: EMBL:X51344; NID:g61993; PIDN:CAA35727.1; PID:g908898
 C:Genetics:
 A:Genetic code: SGC3

Query Match 1.4%; Score 7; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 VLLVAAI 440
 |||||

Db 5 VLLVAAI 11

RESULT 15

G97758
Hypothetical protein RC0471 [Imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: G97758
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: G97758
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <KUR>
A:Cross-references: GB:AF006914; FIDN:AAL03009.1; PID:gl5619544; GSPDB:GN00173
C:Genetics:
A:Gene: RC0471

Query Match 1.48; Score 7; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 IELDPSK 289

||||||

Db 16 IELDPSK 22

Search completed: April 22, 2003, 16:19:38
Job time : 67 secs

QY 58 PDRTOIS-----QDLGGCTLAMDTLPDNRTRVVEDN--HSYVSRLY--GPSEPHS 104
 Db 94 LRQDMLAHAKGMSLVQDLVGADQENALP---TRVTFEFAWHSLFIRNLLIRPPREGLA 150
 QY 105 RELWVDVAEANSRQVKIHTILSNTHQASR--VLSFDFPFYGHPLROITATGGTFIMG 162
 Db 151 SFU-----PKLTIIDLSFRANPERHCRGETIIACD-----LTKGLVLIGTYSVAG 197
 QY 163 DVIHRLMTATQYVAP-----LMANFNGYSDNSTVYVF-----DNGTFV 202
 Db 198 EMKKSFTVLNLYLLENKAMPVHCSANVGPA---GDTAIFPGLSGTGKTTLSADPNRTLI 254
 QY 203 VQMDHVLYQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKYTGSLDAFMI 262
 Db 255 GDDHE-----GWSKGVNFEG-----GCYAKAIRLSEAAPEIFEATRRFGTVMENVVLD 305
 QY 263 LNPSPDVPESSRRRSIFEYHRIELDFSKVTSMSAVEFTPLPTCLQHRSCDA 312
 Db 306 ERRAPDFONG---SLTENTRIAYPLDFIPNASEGTAPQPTIIMLTADA 352

RESULT 2
 ID PCK_RHIME STANDARD; PRT; 536 AA.
 AC P43085;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP
 DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).
 GN PCKA OR R00045 OR SMC02562.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-SU47 / 1021.
 RX MEDLINE=95189720; PubMed=7883700;
 RA Oesteras M., Driscoll B.T., Finan T.M.;
 RT "Molecular and expression analysis of the Rhizobium meliloti
 RT phosphoenolpyruvate carboxylase (pckA) gene.";
 RL J. Bacteriol. 177:1452-1460(1995).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=1021.
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe P., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
 CC + CO(2).
 CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 CC FAMILY.

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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U15199; AAA69973.1;
 CC DR EMBL; AL591782; CAC41432.1;
 CC DR HSSP; P22259; IAQ2.

DR InterPro: IPR001272; PEPCK_ATP.
 DR Pfam: PF01293; PEPCK_ATP; 1.
 DR ProDom: PD004723; PEPCK_ATP; 1.
 DR TIGRfam: TIGR00224; pckA; 1.
 DR PROSITE: PS00532; PEPCK_ATP; 1.
 KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.
 FT NP_BIND 236 243 ATP (BY SIMILARITY).
 SQ SEQUENCE 536 AA; 58119 MW; 1A0F7CEE6C3EBAED CRC64;

Query Match 3.8%; Score 102; DB 1; Length 536;
 Best Local Similarity 20.6%; Pred. No. 0.91;
 Matches 63; Conservative 39; Mismatches 134; Indels 70; Gaps 12;

QY 44 WNRARSPCHVSEPTDRTOLS-----QDLGGCTLAMDTLPDNRTRVVEDN--HSY 92
 Db 80 WDNNSAISPEHFEVLRRDMLAHAKGMSLVQDLVGADPENALP---TRVTFEFAWHSLF 136
 QY 93 VSLYGPSPHSRELW-----VDVAEANSRQVKIHTILSNTHQASRVLSFDFPFYGH 146
 Db 137 IRNLLIRPEREALPSFQPKLTIIDLPSEKADPVR-----HGCRSETVIACD----- 182
 QY 147 PLRQITATGGFTFMGCVIHRMLTATQYVAP-----LMANFNGYSDNSTVYVF--- 195
 Db 183 -LTNGLVLIGGTSYAGEMKKSFTVLNLYLPEKSYMPMHCSANVGPA---GDTAIFGLS 238
 QY 196 -----DNGTFVYQWHDVLYQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEIS 246
 Db 239 GTGKTTLSADPNRTLIGDDEH---GWSEKGVNFEG-----GCYAKAIRLSEAAPEIF 289
 QY 247 SQQHPVKYTGSLDAFMIINPSPDVPESSRRRSIFEYHRIELDFSKVTSMSAVEFTPLPTCLQ 306
 Db 290 ATTRFGTVMENVVLDERRLPDDEG---SLTENTRCAYPLHFIPNASKTGTAPOPTII 346
 QY 307 HRSCDA 312
 Db 347 MLTADA 352

RESULT 3
 ID SMC6C_RAT STANDARD; PRT; 960 AA.
 AC Q9WTL3; Q9WTL6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SDRague-Dawley; Tissue=Muscle;
 RX MEDLINE=99160821; PubMed=10049528;
 RA Kikuchi K., Chedotal A., Hanafusa H., Ujima Y., de Castro F.,
 RA Goodman C.S., Kimura T.;
 RT "Cloning and characterization of a novel class VI semaphorin,
 RT semaphorin Y.";
 RL Mol. Cell. Neurosci. 13:9-23(1999).
 CC -1- FUNCTION: SHOWS GROWTH CONE COLLAPSING ACTIVITY ON DORSAL ROOT
 CC GANGLION (DRG) NEURONS IN VITRO. MAY BE A STOP SIGNAL FOR THE DRG
 CC NEURONS IN THEIR TARGET AREAS, AND POSSIBLY ALSO FOR OTHER
 CC NEURONS. MAY ALSO BE INVOLVED IN THE MAINTENANCE AND REMODELING OF
 CC NEURONAL CONNECTIONS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SEMA Y-L (SHOWN HERE) AND SEMA
 CC Y-S; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY REGIONS OF THE DEVELOPING
 CC NERVOUS SYSTEM, PROBABLY IN NEURONS AND THEIR PRECURSORS, BUT ALSO
 CC IN NONNEURAL TISSUE SUCH AS IMMATURE MUSCLE AND DERMIS. IN ADULT,
 CC STRONG EXPRESSION IN THE SKELETAL MUSCLE AND MODERATE EXPRESSION
 CC IN THE BRAIN, WHERE CEREBELLUM SHOWS THE HIGHEST EXPRESSION. ALSO

EXPRESSED IN ALMOST ALL AREAS OF THE CNS.
 -!- DEVELOPMENTAL STAGE: DETECTED AT E12 AND FOUND AT MARKEDLY
 INCREASED LEVELS AT E15 AND E18 IN BOTH THE HEAD AND THE BODY. AT
 BIRTH THE LEVEL DECREASES SIGNIFICANTLY.
 -!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 -!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.

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 EMBL; AB000817; BAA76293.2; -;
 DR EMBL; AB014074; BAA76295.1; -;
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 960 SEMAPHORIN 6C.
 FT DOMAIN 24 635 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 636 656 POTENTIAL.
 FT DOMAIN 657 960 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 541 SEMA.
 FT DOMAIN 693 699 POLY-PRO.
 FT DOMAIN 783 786 POLY-PRO.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 586 617 MISSING (IN ISOFORM SEMA Y-S).
 SQ SEQUENCE 960 AA; 102610 MW; C88293C5607E6086 CRC64;

 Query Match 3.8%; Score 102; DB 1; Length 960;
 Best Local Similarity 19.1%; Pred. No. 2;
 Matches 105; Conservative 60; Mismatches 173; Indels 212; Gaps 27;
 QY 17 RALSPQ---GAGHDEPGSGWAAAGTVGVGNWR-----ARESPGHV-----SE 57
 DB 202 RSLGPPPLRSKAYS-----KWLREPHFVVALEHGDHVVFFREVSVEDAR 248
 QY 58 PRTQLS-----QDLGGTILMD-----TLDPNRTVRVEDNHSYV---VS 94
 DB 249 LGRVFSRVARVCKRDMGSPRALDRHWTSLKRLNCSVPGDST-----FYFDVLQ 300
 QY 95 RLYGFSEPHSRE-----ANRQVKIHTLNTHQASRVVLSDFDFYGHPLRQIYIATGFTMGDV 112
 DB 301 SLTGPVNLHGRSALFGVFTTQNSIPGSAVCAFYLDLTERGPEGFKQRSILDGAWTPVS 360
 QY 113 E-----ANRQVKIHTLNTHQASRVVLSDFDFYGHPLRQIYIATGFTMGDV 164
 DB 361 EDKVPSPRGSCAGVGAALFSSODLPDVLFLFK-----AHPLLDPVAVP-----PA 408
 QY 165 IHR---MLTATQVAPLMANPNPGYSDNSTVYVF---DNGTVFVQWHDVYLGWEDKGSF 219
 DB 409 THQPLTLTSLRALLTOVAVDGMAGPHRNTVILFSGNDGTVL-----KVLPPGGSLG-- 461
 QY 220 TFOAALHHDGRIVFAYKEIPMSYPEISSSQHEPVKTLGSDAFMLNPNPDPVPSRRRSIFE 279
 DB 462 -----PEPIILEEDIDAYSHARCSKRS-----PRAARRIL-- 491
 QY 280 YHRIELDPK-----VYMSAVFETPLPTCLQRSDACAMSSDLTFNCMSCHVQRC----- 331
 DB 492 --GLELDTGHRFLFAFPGCIIVYLSLRCAHGAQORSLASLDPCYCGW-HRFRGCVNIR 548
 QY 332 -SSGFD---RYRQEMDYG-CAQEAQRMCEDFQDEHDSA-----SPDTSFSPVDG 378
 DB 549 GPGGTVDLTNGOESMEHGDQDQATGS-----QSGPGDSAYVLLGPGSPETPSPSDA 603
 QY 379 DLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNISPKTKGTPVHLGTIVGTIVLAVLVA 438
 DB 379 DLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNISPKTKGTPVHLGTIVGTIVLAVLVA 438

DB 604 HPGPQSSTL-----GAHTQGVRRDLSPASASRSIPIPIILLACVAAAFALG 648
 QY 439 AILLAGIYN 448
 DB 649 ASV-SGLLV 657

 RESULT 4
 GLI3_XENLA STANDARD; PRT; 1569 AA.
 ID GLI3_XENLA
 AC Q91660;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein GLI3 (Neural specific DNA binding protein XGLI3)
 DE (XGLI-3).
 GN GLI3.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97346726; PubMed=9203143;
 RA Marine J.C., Bellefroid E.J., Pendeville H., Martial J.A., Pieler T.;
 RT "A role for Xenopus Gli-type zinc finger proteins in the early
 embryonic patterning of mesoderm and neuroectoderm";
 RL Mech. Dev. 63:211-225(1997).
 CC -!- FUNCTION: HAS AN ESSENTIAL ROLE IN THE EARLY EMBRYONIC PATTERNING
 OF MESODERM AND NEUROECTODERM. IMPLICATED IN THE TRANSDUCTION OF
 SHH SIGNAL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
 PROTEINS.
 CC -----
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 EMBL; U42461; AAA98466.1; -;
 DR HSP; P08151; ZGLI.
 DR InterPro; IPR000822; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR SMART; SM00355; Znf_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2.1; 4.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2.2; 5.
 KW Zinc-finger; Metal-binding; DNA-binding; Transcription regulation;
 KW Nuclear protein; Repeat.
 FT DOMAIN 485 637 ZINC FINGERS.
 FT ZN_FING 485 510 C2H2-TYPE.
 FT ZN_FING 518 545 C2H2-TYPE.
 FT ZN_FING 551 575 C2H2-TYPE.
 FT ZN_FING 581 606 C2H2-TYPE.
 FT ZN_FING 612 637 C2H2-TYPE.
 SQ SEQUENCE 1569 AA; 172594 MW; 71F5DC117A930B82 CRC64;

 Query Match 3.8%; Score 101.5; DB 1; Length 1569;
 Best Local Similarity 20.9%; Pred. No. 4.4;
 Matches 48; Conservative 29; Mismatches 70; Indels 83; Gaps 10;
 QY 187 SDNFTVYVDFGVVQWHDVHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSV--- 242
 DB 316 SPNSLVITLNSR-----SSSSASCSYGLHAASAPALNAYQPTPVSLQOMH 364
 QY 243 PEISSQHPVKTLGSDAFMLNPNPDPVPSRR-----RSIFYHRIELDP-----KVTS 292
 DB 365 QQIMSRQHSIGSAGFCHSPPLLHPAPTFPSQRTIPGIFSVLNPVQVSGPSEAAQNKPTS 424

QY 293 MSABFT-----PUPCTCLOHR-----SCDACMSSDLTF- 320
 DB 425 ESASVSTGDLHNRKSKVPEDHPSPGAVCIQDPDGMTLVKEGVKDESKQAEVYVE 484
 QY 321 -NCSCWHLORCSSGFDYRQ-----EMWDYGAQAE 350
 DB 485 TNCHW-----EGCSREFDQEQVLVHHNNDHITHGKKEFVCRWLD--CSRE 528

RESULT 5

ID PCK_RHILO STANDARD; PRT; 536 AA.
 AC Q96CL7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP
 DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).
 GN PCKA OR MRS096.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
 CC + CO(2).
 CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 CC FAMILY.

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EMBL; AP003005; BAB51604.1; -
 DR InterPro; IPR001272; PEPCK_ATP.
 DR Pfam; PF01293; PEPCK_ATP.1.
 DR ProDom; PD004723; PEPCK_ATP.1.
 DR TIGRFAMs; TIGR00224; pckA.1.
 DR PROSITE; PS00532; PEPCK_ATP; FALSE_NEG.
 KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.
 FT NP_BIND 236 243 ATP (BY SIMILARITY).
 SQ SEQUENCE 536 AA; 8A3E5D3C7E290743 CRC64;

Query Match 3.7%; Score 99.5; DB 1; Length 536;
 Best Local Similarity 23.0%; Pred. No. 1.5;
 Matches 61; Conservative 37; Mismatches 104; Indels 63; Gaps 14;

QY 44 WNRARESP-----GHVSEPDRTQLSDGGGTAMDLPDNRTRVVEDN--HS 90
 DB 80 WDNKATSPAQETLPADFALAHAKND--LYVDLVGGDAEALKLP---TRVTEFAWHS 134
 QY 91 YVVSRLYGPSEPHSRLWVDVAENRSQVKHITLNSNTHQASR--VWLSFDFFPYGHPL 148
 DB 135 LFIKNLL--IRPKAELGQVPE--MTIIDLPFRADPARHGRSTETVIAVDL-----T 184

QY 149 RQTIATGGFIEMGDVHRMLTATQY-----VAPLMANFNPCYSDNSTVVFNDGT--- 199
 DB 185 RQI-VLIGTSVAGENKKSVFTMLNVLKQGVMPHCSANEGPAGDAVFFGLSGTGT 243
 QY 200 -----VFVQVDHIVYLOGHEDKGSFTFOAALHHDGRIVFAYKEIPMSV--*PEISS 248
 DB 244 TUSADPSRTLIGDDEH---GMGPHGIFNEFGCY-----AKTIKLSAAEPEIFAT 291
 QY 249 QHPVKTGLSDAFMLNPSDPVPESR 273
 DB 292 TQRFGTVLNVLDADGVDFNDGR 316

RESULT 6

ID N170_YEAST STANDARD; PRT; 1502 AA.
 AC P38181;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Nucleoporin NUP170 (Nuclear pore protein NUP170).
 GN NUP170 OR YBL079W OR YBL0725
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RX MEDLINE=96076635; PubMed=7502586;
 RA Obermaier B., Gassenhuber J., Piravandi E., Domdey H.;
 RT "Sequence analysis of a 78.6 kb segment of the left end of
 RT Saccharomyces cerevisiae chromosome II.";
 RL Yeast 11:1103-1112(1995).
 RN [2]
 RP SEQUENCE OF 1262-1502 FROM N.A.
 RC STRAIN=S288c;
 RA Contreras R., Fiers W., Logghe M., Molemans F.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION, AND SEQUENCE OF 117-133 AND 153-166.
 RX MEDLINE=96095775; PubMed=8522578;
 RA Aitchison J.D., Rout M.P., Marelli M., Blobel G., Wozniak R.W.;
 RT "Two novel related yeast nucleoporins Nup170p and Nup157p:
 RT complementation with the vertebrate homologue Nup155p and functional
 RT interactions with the yeast nuclear pore-membrane protein Pom152p.";
 RL J. Cell Biol. 131:1133-1148(1995).
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear pore complex.
 CC -!- SIMILARITY: TO YEAST NUP157, AND SOME, TO MAMMALIAN NUP155.

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EMBL; X79489; CAA56029.1; -
 DR EMBL; Z35840; CAA84900.1; -
 DR PIR; S45429; S45429.
 DR SGD; S0000175; NUP170.
 DR InterPro; IPR004870; Nup_nucleoporin.
 DR Pfam; PF03177; Nucleoporin; 1.
 KW Nuclear protein; Transport.
 SQ SEQUENCE 1502 AA; 169474 MW; 3BEA65DAA2A5F99A CRC64;

Query Match 3.6%; Score 98; DB 1; Length 1502;
 Best Local Similarity 22.7%; Pred. No. 8.2;
 Matches 62; Conservative 41; Mismatches 106; Indels 64; Gaps 14;

QY 61 TQLSQDLGGGTAMDLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQVK 120

DB 778 TELLRLDINGRHEVEM-TFTDNRV-----TSHAFISS--DPITPSNNLKSDEISQNRNII- 829
 QY 121 IHTILSNTHROASRVLSFD-PPYGHPLROITATGCFIPMGDVIHRLMTATQYVAP-L 178
 DB 830 -----SKVSTSKDCIEY---LSSINILNEFFITYGDSI-----SQISAPYV 868
 QY 179 MANFNPGYSDNSTVVYFD-----NGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRI 231
 DB 869 LANNNGRVRIDKTEVANAQSAIALNMIKMQV-----SIKEGLSEFLNLYEYSEV 919
 QY 232 -----VFAYKEIPMSVPEISSQHPVKTLGSDAFMLNPSDPVPESSRRISEYHRIEL 285
 DB 920 EGFNOYLQCFKDI-ISFVSLDVQKDLVKLDFKDLF-----APNDKTKSLIREILLSI 970
 QY 286 DPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 318
 DB 971 INRNITKASIEYT--ATALQERCGSFCSASDI 1001

RESULT 7
 ID PLX4_HUMAN STANDARD; PRT; 1871 AA.
 AC P51805;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plexin A3 precursor (Plexin 4) (Transmembrane protein sex).
 GN PLXNA3 OR PLXNA4 OR SEX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain, Skeletal muscle, and Embryo;
 RX MEDLINE=96149362; PubMed=8570614;
 RA Bione S., Tamagnone L., Longati P., Cremona O., Gullisano M.,
 RA Bione S., Tamagnone F., Neel B.G., Toniolo D., Conoglio P.M.:
 "A family of transmembrane proteins with homology to the MET-
 hepatocyte growth factor receptor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:674-678(1996).
 RL CC -!- FUNCTION: PUTATIVE RECEPTOR INVOLVED IN THE DEVELOPMENT OF NEURAL
 CC AND EPITHELIAL TISSUES.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: PREDOMINANT IN NEURAL TISSUE DURING
 CC DEVELOPMENT (BY SIMILARITY); WIDELY EXPRESSED IN ADULT TISSUE.
 CC -!- SIMILARITY: WITH THE EXTRACELLULAR DOMAIN OF THE MET/ROH/HGF
 CC RECEPTORS AND THE CYTOPLASMIC DOMAIN OF SEP, NOV AND OCT.
 CC
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 CC
 CC EMBL; X87852; CA61132.1; -
 CC Genew; HGNC:9101; PLXNA3.
 CC MIM; 300022; -
 CC InterPro; IPR002909; IPT_TIG.
 CC InterPro; IPR003659; Plexin-like.
 CC InterPro; IPR002165; Plexin_repeat.
 CC InterPro; IPR001627; Sema.
 CC Pfam; PF01403; Sema; 1.
 CC Pfam; PF01437; PSI; 3.
 CC Pfam; PF01833; TIG; 4.
 CC SMART; SM00429; IPT; 4.
 CC SMART; SM00423; PSI; 3.
 CC Receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 19 POTENTIAL.
 FT SIGNAL 20 1871 PLEXIN A3.
 FT CHAIN

FT DOMAIN 20 1220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1221 1241 POTENTIAL.
 FT DOMAIN 1242 1871 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 738 738 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 746 746 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1009 1009 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1036 1036 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1073 1073 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1115 1115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1162 1162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1871 AA; 207661 MW; 28420CEBDB22E9CE CRC64;

Query Match 3.6%; Score 98; DB 1; Length 1871;
 Best Local Similarity 24.2%; Pred. No. 11;
 Matches 43; Conservative 25; Mismatches 58; Indels 52; Gaps 10;

QY 160 FMGDVIHRLMTATQYV--APLMANFNPGYSDNSTVVYFDNGTVFV----VQMDHVYVLOGW 213
 DB 386 FCGLVLNQPLGGLHVEICGLPLADSTDGMSVAAYTYRQHSVVFICTRSGSLKKVRVDGF 445
 QY 214 EDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSDAFMLNPSDPVPESR 273
 DB 446 QD-----AHLVE-----TVPVVDGS--PI---LRDLFF----SPD----- 471
 QY 274 RRSIFEYHRIELDPKSVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLCORC 331
 DB 472 HRIHY-----LLSEKQVSQLPVTCEQYQCAACLGSG-DPHCGMCLVRHRC 517

RESULT 8
 ID IRFL_CHICK STANDARD; PRT; 313 AA.
 AC Q90876;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interferon regulatory factor 1 (IRF-1).
 GN IRF1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95241453; PubMed=7536924;
 RA Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U.;
 RA David I.B.;
 RT "Chicken interferon consensus sequence-binding protein (ICSBP) and
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
 RT conservation in the IRF gene family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
 CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
 CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE IRF FAMILY.
 CC
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 CC
 CC EMBL; L39766; AAA62160.1; -
 CC HSPP; P15314; IIF1.
 CC InterPro; IPR001346; IRF.

Best Local Similarity 23.0%; Pred. No. 11;
Matches 38; Conservative 23; Mismatches 55; Indels 49; Gaps 7;
QY 275 RSIFYHRELDPSKVTSMASVEFTPLPCLQHRSCDACMSDLTFNC--SHC----- 325
Db 639 KSLFNRAEQPEPRSVSSVS-QFS-----DAAQSPSSSSPSCPEPAQAN 686
QY 326 -----HVLQRCSSGFDYRQEWMDYGCQAEGRMCEQFQDRDHDSASPD 370
Db 687 MDISTGHMILAYMEDHLNR-----DRLAKEWQAL-CAVQAEPTNCAAAQDESNTKKNRH 740
QY 371 TSFSPVDG-----DLTTSSSLFDISLTTEDDKLNPAYGGG 408
Db 741 PDLPLVDHARIKLKVESSPSRSDYNASPIIEHDPMPAYIATQG 785

RESULT 14

PPCK BRUME
ID PPCK BRUME STANDARD; PRT; 536 AA.
AC Q8YE41;
DT 15-JUN-2002 (Rel. 41, Last Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP
DE carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
GN PCKA OR BMEI2037.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Ilevicchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jankovskii L., Larsen N., D'Souza M., Bernal A., Mazur M., Golsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kypides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Coudert E.;
RL Unpublished observations (MAY-2001).

CC -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
CC + CO(2).
CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
CC FAMILY.
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A STOP CODON IN
CC POSITION 492 WAS TRANSLATED AS TRP TO RESTORE THE SIMILARITY WITH
CC THE C-TERMINAL REGION OF OTHER HOMOLOGS.
CC
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CC EMBL: AE009636; AAL53218.1; ALT_TERM.
CC InterPro: IPR001272; PEPCK_ATP.
CC Pfam: PF01293; PEPCK_ATP_1.
CC TIGRFAMs: TIGR00224; pckA; 1.
CC PROSITE: PS00532; PEPCK_ATP; 1.
CC Gluconeogenesis; Lyase; Decarboxylase; Complete proteome.
CC NP_BIND 236 243 ATP (BY SIMILARITY).
CC SEQUENCE 536 AA; 58598 MW; 8EC32A1A99FCEA5F CRC64;

Query Match 3.5%; Score 93; DB 1; Length 536;
Best Local Similarity 22.4%; Pred. No. 5.1;
Matches 64; Conservative 41; Mismatches 95; Indels 86; Gaps 15;
QY 65 QDLGGGTAMDTPDNR--TRVEDN--HSYVV--SRLYGPSEPHSRELWVDVAEANSQV 119
Db 110 QDLGGGADA-----DNKINARVITEYAWHSILFIRNLIRPSQ-----EALASYV 153
QY 120 KIHTILSNTHQA-----SRVLSDFPFYGHPLRQITATGTFIFMGDVHRLMTA 171
Db 154 PEMTIIDLPSCADPERYGVRTETVIAV-----LTRKIVLIGGTSYAGEMKKSFTFA 206
QY 172 TQY-----VAPLMANPNPGYSDNSTVYFDNGT-----VFVQWDHVYLOGWE 214
Db 207 LNYILPAKGYWPHCSANEGPNGDTAVFFGLSGTGKTTLSADPTRTLIGDDEH----GWG 262
QY 215 DKSFTFOAALHHDGRIVFAYKEIPMSV-----PEISSQHPVKTLGSDAFMLNPSDPVE 271
Db 263 EHGYNFEGGCY-----AKTIRLSAAEPEIYATTQRFGTVLENVVLNDRQPDDED 314
QY 272 SRRRSIFEYHR--IELD-----PSKVTSMASVEFTPLP 302
Db 315 G---SLTENTRCAYPLDPIPNASKSGKGQPKNIIMLTADAFGVMP 357

RESULT 15

IFH1_YEAST
ID IFH1_YEAST STANDARD; PRT; 1085 AA.
AC P39520;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE IFH1 protein (RRP3 protein).
GN IFH1 OR RRP3 OR YUR223C OR L8083.9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=95304839; PubMed=7785326;
RA Cherel I., Thuriaux P.;
RT "The IFH1 gene product interacts with a fork head protein in
RT Saccharomyces cerevisiae.";
RL Yeast 11:261-270(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favella A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevisakis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONTROLS THE PRE-RRNA PROCESSING MACHINERY IN
CC CONJUNCTION WITH FHL1. COULD CONVERT FHL1 FROM A REPRESSOR
CC TO AN ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC
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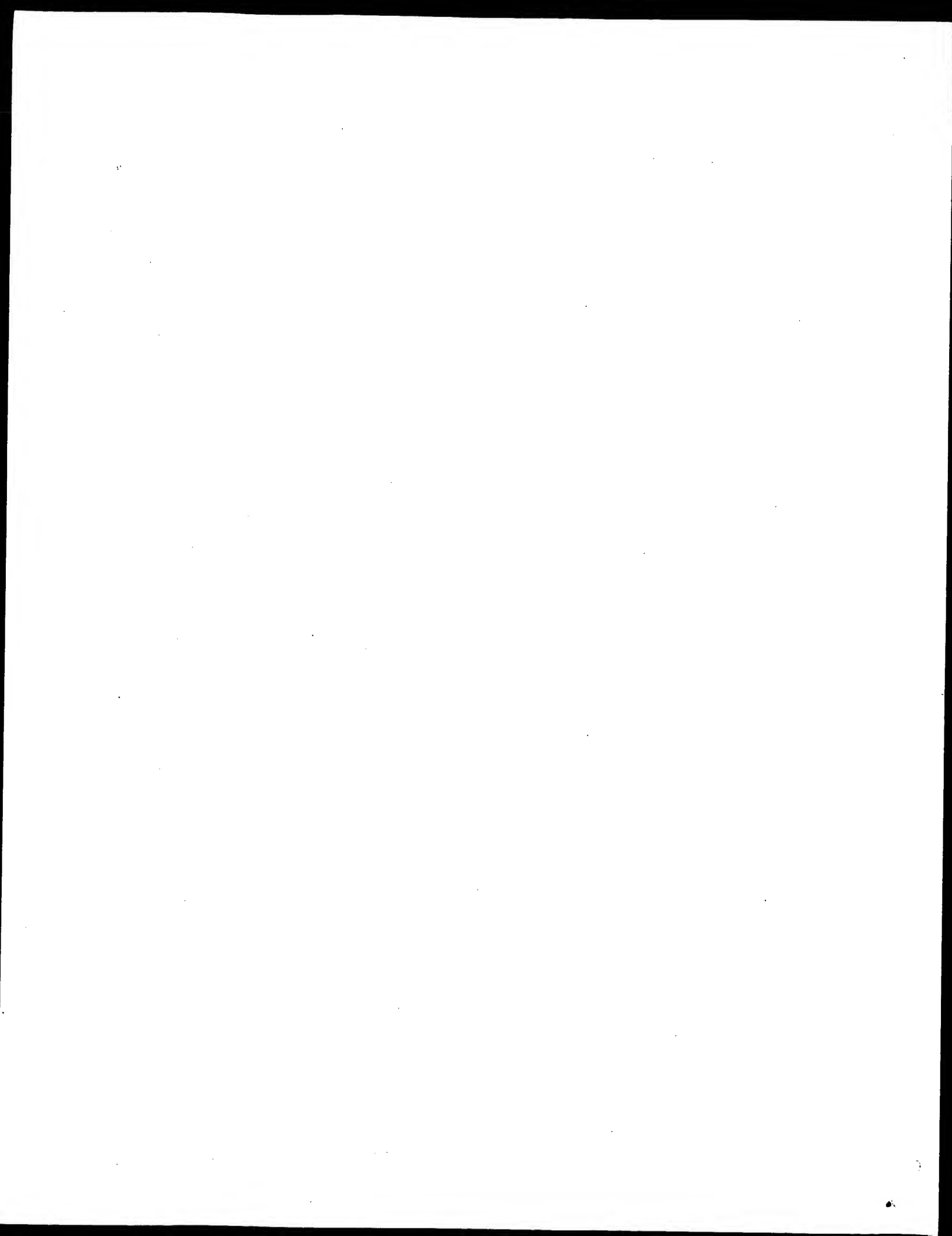
CC EMBL: Z29488; CAA82624.1; -;
CC EMBL: U19027; AAB67412.1; -;
CC PIR: S47477; S47477.

DR SGD; S0004213; IFH1.
 KW Nuclear protein; Transcription regulation.
 FT DOMAIN 122 163 ASP/GLU-RICH (HIGHLY ACIDIC).
 SQ SEQUENCE 1085 AA; 122491 MW; BE1C7DEF06213FE0 CRC64;

Query Match 3.5%; Score 93; DB 1; Length 1085;
 Best Local Similarity 19.0%; Pred. No. 14;
 Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY	56	SEPDRQLSGLGGGTFLAMDTLPDNRTRVVDNHSYVYVRLYGPSPHSHRELWVD--VAE	113
Db	333	NEDSHGEIGTDLTGE---DDLPL---LLEEEQNIYSEL-----QNDELSEFGSLHE	379
QY	114	ANRSQVK--IHTILSNTHQAS-----RVVLSDFPFYGHPLRQIITATGGFIFM	161
Db	380	EGSDPVEDAEKFLQNEYQNGYDEDEDEDEIMSDFMPEYEDP-----KFNALYYY	433
QY	162	GDVHRLMTATQYVAPLMA-----FNPGYSDNST	191
Db	434	GDGSEPKLSLSTSL-PLMLNDEKLSKLLKKEAKKREQERKORRKLKKTOKPSTRITSN	492
QY	192	VVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVPAYK-----EIPMSVPEISS	247
Db	493	V---DNDEYIF---NVFQSDDENSGHKSGKGRHKSKEHKNKGSNLKSNDDLEP	545
QY	248	SQHP--VKTGLSFAFMILNPDVPESSRRSIFEYHRIELDPFSKVTSMASAVEFTPLTCL	305
Db	546	STHSTVLNSGKYDS-----SDD-----EYDNILLD-----VAHMP-----	575
QY	306	QHRSCDACMSDLTFNCWCHVLQRCSSGDFRYRQEWMDYGCQAEGRAEGRMCEDFQDEHDH	365
Db	576	---SDDECSSESTSHDADTEELRALDS-----DSLIGT-----ELDDDYEDDDDD	619
QY	366	SA-----SPDTFSFSDYDGD---LTTTSSS-----LFIDSL	392
Db	620	SSVTNVFIDIDDLDPDSFYHYDSDGSSSLISSNSDKENSGDKCKKHDLLETIVVYVDDE	679
QY	393	TTEDDTKLINPYAGDGLQNNLSPKTKG-----TPVHLGT	426
Db	680	STDEDDNLPP---PSSRSKNIGSKAKEIVSNVYGLRPPKLG	719

Search completed: April 22, 2003, 16:07:09
 Job time : 31 secs



GenCore version 5.1.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:08:50 ; Search time 14 Seconds
(without alignments)
1481.297 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 500
Sequence: 1 MRGELWLLVLRARALS.....YAEVPSGHEKGFMEADQC 500

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.6	429	1 ARSB_STAUAU	P30329 staphylococ
2	7	1.4	75	1 VE5_HPV33	P06426 human papil
3	7	1.4	76	1 VE5_HPV58	P26552 human papil
4	7	1.4	78	1 VG9_SPV1R	P15900 spiroplasma
5	7	1.4	106	1 VMEM_CVB	P37989 chrysanthem
6	7	1.4	120	1 GADP_PIG	Q91295 sus scrofa
7	7	1.4	225	1 VMEL_IBV6	P05136 avian infec
8	7	1.4	225	1 VMEL_IBV2	P04327 avian infec
9	7	1.4	225	1 VMEL_IBV6	P11222 avian infec
10	7	1.4	225	1 VMEL_IBV6	P12649 avian infec
11	7	1.4	237	1 VG16_BPHC	Q92x92 bacterioph
12	7	1.4	286	1 YCXE_BACME	P40419 bacillus me
13	7	1.4	342	1 V084_HSV60	P52532 human herpe
14	7	1.4	372	1 INVE_SALTY	P35671 salmonella
15	7	1.4	388	1 FTSW_HELPJ	Q92748 helicobacte
16	7	1.4	388	1 FTSW_HELPJ	P56096 helicobacte
17	7	1.4	397	1 S17A_RABIT	Q9gm70 oryctolagus
18	7	1.4	401	1 HUTI_CAUCR	P58079 caulobacter
19	7	1.4	407	1 HUTI_AGRRH	Q9kwe5 agrobacteri
20	7	1.4	409	1 HUTI_RHIME	Q98311 rhizobium l
21	7	1.4	415	1 HUTI_RHIME	Q31196 rhizobium m
22	7	1.4	417	1 HS47_HUMAN	P29043 homo sapien
23	7	1.4	417	1 HS47_MOUSE	P19324 mus musculu
24	7	1.4	417	1 HS47_MOUSE	P29457 rattus norv
25	7	1.4	418	1 CBP2_HUMAN	P50454 homo sapien
26	7	1.4	430	1 SPAL_SHIFL	P35531 shigella fl
27	7	1.4	471	1 STCH_HUMAN	P48723 homo sapien
28	7	1.4	472	1 CB1R_FELCA	O02777 felis silve
29	7	1.4	473	1 CB1R_MOUSE	P47746 mus musculu
30	7	1.4	473	1 CB1R_POEGU	P56971 poephila gu
31	7	1.4	473	1 CB1R_RAT	P20272 rattus norv
32	7	1.4	498	1 LYXK_ECOLI	P37677 escherichia
33	7	1.4	524	1 PIF3_ARATH	O80536 arabidopsis

1	Y322_MYCGE	1	558	1	1.4	7	34
2	DTXH_CORBE	1	560	1	1.4	7	35
3	DTX_COROM	1	560	1	1.4	7	36
4	DTX_CORBE	1	567	1	1.4	7	37
5	DNAX_METTH	1	596	1	1.4	7	38
6	DNAX_THEAC	1	613	1	1.4	7	39
7	DNAX_THEVO	1	613	1	1.4	7	40
8	YG4P_YEAST	1	622	1	1.4	7	41
9	Y481_HUMAN	1	650	1	1.4	7	42
10	CAOI_HUMAN	1	660	1	1.4	7	43
11	DP3E_RHOCA	1	704	1	1.4	7	44
12	DNAX_APHHA	1	721	1	1.4	7	45
13	CADC_HUMAN	1	794	1	1.4	7	46
14	SGS_HUMAN	1	826	1	1.4	7	47
15	YDGH_BACSU	1	885	1	1.4	7	48
16	PTP3_DICDI	1	989	1	1.4	7	49
17	YB85_YEAST	1	1120	1	1.4	7	50
18	CIHA_BACTU	1	1172	1	1.4	7	51
19	NRX1_BOVIN	1	1216	1	1.4	7	52
20	LYS5_ECOLI	1	47	1	1.2	6	53
21	LYS7_ECOLI	1	47	1	1.2	6	54
22	LYS9_ECOLI	1	47	1	1.2	6	55
23	MYRF_METH	1	68	1	1.2	6	56
24	MYRF_METH	1	68	1	1.2	6	57
25	BLE2_STAUA	1	83	1	1.2	6	58
26	RS20_CLOPE	1	87	1	1.2	6	59
27	PTHP_NEIMA	1	89	1	1.2	6	60
28	GAC1_CLOAB	1	95	1	1.2	6	61
29	YBGA_THEMEA	1	98	1	1.2	6	62
30	APC3_WACFA	1	99	1	1.2	6	63
31	APC3_CANFA	1	100	1	1.2	6	64
32	DEF6_HUMAN	1	100	1	1.2	6	65
33	RL4_PIG	1	101	1	1.2	6	66
34	Y70A_METUA	1	102	1	1.2	6	67
35	VMEM_SMYPEA	1	108	1	1.2	6	68
36	YJFP_BACSU	1	109	1	1.2	6	69
37	HS70_HYDOL	1	111	1	1.2	6	70
38	YFBW_ECOLI	1	111	1	1.2	6	71
39	YFBW_SALTY	1	111	1	1.2	6	72
40	NRG4_MOUSE	1	111	1	1.2	6	73
41	NLT2_BRANA	1	115	1	1.2	6	74
42	NLT1_ARATH	1	117	1	1.2	6	75
43	NLTD_BRAOL	1	118	1	1.2	6	76
44	FOLX_ECOLI	1	118	1	1.2	6	77
45	ACPM_ARATH	1	119	1	1.2	6	78
46	YK63_MYCTU	1	122	1	1.2	6	79
47	VGL1_PPA	1	124	1	1.2	6	80
48	CD59_PAPSP	1	126	1	1.2	6	81
49	NRML_RAT	1	126	1	1.2	6	82
50	SECE_VTBCH	1	126	1	1.2	6	83
51	VG41_HAEIN	1	127	1	1.2	6	84
52	CD59_CERAE	1	127	1	1.2	6	85
53	POLG_HCVCE	1	128	1	1.2	6	86
54	SODM_MYCCE	1	138	1	1.2	6	87
55	SODM_MYCMR	1	138	1	1.2	6	88
56	SODM_MYCSZ	1	138	1	1.2	6	89
57	RBS_OLILU	1	139	1	1.2	6	90
58	TOLR_HAEIN	1	139	1	1.2	6	91
59	GLB1_LUCPE	1	142	1	1.2	6	92
60	RS6_RHOCA	1	144	1	1.2	6	93
61	AR15_CAEEL	1	146	1	1.2	6	94
62	PA21_PIG	1	146	1	1.2	6	95
63	LYC_COTJA	1	147	1	1.2	6	96
64	PA21_HUMAN	1	148	1	1.2	6	97
65	RNP_TATNG	1	148	1	1.2	6	98
66	RNP_TATNG	1	148	1	1.2	6	99
67	RNP_CAUCR	1	149	1	1.2	6	100
68	RNP_ACOCA	1	149	1	1.2	6	101
69	RNP_LEOED	1	149	1	1.2	6	102
70	RNP_NIVCR	1	149	1	1.2	6	103
71	RNP_URARU	1	149	1	1.2	6	104
72	YIDI_ECOLI	1	149	1	1.2	6	105
73	YIDI_ECOLI	1	149	1	1.2	6	106

P47564	mycoplasma
P00589	corynebacter
P00587	corynebacter
P00588	corynebacter
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P00790	corynebacter
P00791	corynebacter
P00792	corynebacter
P00793	coryneb

107	6	1.2	150	1	RNK6_AOTTR	O46528	aotus trivi	180	6	1.2	231	1	YCB2_YEAST	P25556	saccharomyc
108	6	1.2	150	1	RNS_BOVIN	P00656	bos taurus	181	6	1.2	233	1	YA36_METJA	Q58442	methanococc
109	6	1.2	150	1	RNP_BOVIN	P00669	bos taurus	182	6	1.2	235	1	VG48_BPMD2	O64238	mycobacteri
110	6	1.2	150	1	YO24_BHP1	P51726	bacterioph	183	6	1.2	236	1	ALDC_LACIL	P95676	lactococcus
111	6	1.2	152	1	RNP_RAT	P00684	rattus norv	184	6	1.2	236	1	ALDC_LACIL	P77880	lactococcus
112	6	1.2	152	1	RNP_RATRT	Q9wux3	rattus norv	185	6	1.2	238	1	DHSE_ECOLI	P07014	eschlerichia
113	6	1.2	153	1	SORB_PIG	P28220	sus scrofa	186	6	1.2	239	1	HIS4_RHOSH	P50936	rhodobacter
114	6	1.2	153	1	Y721_AGRVI	P70794	agrobacteri	187	6	1.2	243	1	VG48_BPML5	Q05259	mycobacteri
115	6	1.2	156	1	YQ69_MYCTU	P12840	rattus norv	188	6	1.2	244	1	Y399_ARCFU	Q29848	archaeoglob
116	6	1.2	157	1	FCE2_RAT	P12840	rattus norv	189	6	1.2	245	1	FCE1_RAT	P12371	rattus norv
117	6	1.2	159	1	YLH7_CAEEL	P34361	caenorhabd1	190	6	1.2	246	1	MCT9_MOUSE	Q35164	mus musculus
118	6	1.2	161	1	YPMB_ECHGR	P14088	echinococcu	191	6	1.2	246	1	MCT9_MOUSE	Q00356	mus musculus
119	6	1.2	161	1	YPMB_BACSU	P54396	bacillus su	192	6	1.2	247	1	HS77_HUMAN	P48741	homo sapien
120	6	1.2	162	1	PHCA_MASLA	P00307	mastigococc	193	6	1.2	247	1	MCT8_MOUSE	P43430	mus musculus
121	6	1.2	162	1	PHCA_SYNEL	P50032	synthococc	194	6	1.2	251	1	ASTA_ASTFL	P07584	astacus flu
122	6	1.2	163	1	SODM_MYCKA	P50912	mycobacteri	195	6	1.2	251	1	LP3_BOMMO	P09336	bombyx mori
123	6	1.2	164	1	YFB5_YEAST	P43578	saccharomyc	196	6	1.2	254	1	NODJ_AZOCA	O07757	azorhizoblu
124	6	1.2	167	1	RNRB_BOVIN	P39873	bos taurus	197	6	1.2	254	1	RACD_DICDI	P34150	dictyosteli
125	6	1.2	168	1	QX2_SULAC	P39479	sulfolobus	198	6	1.2	255	1	YJ95_MYCTU	Q10863	mycobacteri
126	6	1.2	169	1	HUPJ_BRAJA	P48341	bradyrhizob	199	6	1.2	256	1	ATPF_HUMAN	P24539	homo sapien
127	6	1.2	171	1	NU6M_DRONE	P18933	drosophila	200	6	1.2	256	1	ATPF_MOUSE	Q9C9Q7	mus musculus
128	6	1.2	175	1	T13C_MOUSE	Q9d8d0	mus musculus	201	6	1.2	256	1	ATPF_RAT	P19511	rattus norv
129	6	1.2	176	1	AROK_CHLPN	Q9d8d0	mus musculus	202	6	1.2	256	1	L301_BOMMO	Q08002	bombyx mori
130	6	1.2	182	1	K2C4_BOVIN	P04260	chlamydia p	203	6	1.2	258	1	SSEB_ECOLI	P31143	eschlerichia
131	6	1.2	182	1	MCRC_METVO	P11567	methanococc	204	6	1.2	260	1	VP33_APLCA	P16843	aplysia cal
132	6	1.2	185	1	PSAF_PORRU	P51193	porphyra pu	205	6	1.2	261	1	GLDI_HUMAN	P56856	homo sapien
133	6	1.2	185	1	VCO7_ADE40	Q89532	human adeno	206	6	1.2	261	1	GSHI_MOUSE	P31315	mus musculus
134	6	1.2	189	1	Y006_CHLTR	O84009	chlamydia t	207	6	1.2	261	1	RNG6_HUMAN	P28067	homo sapien
135	6	1.2	190	1	Y2H5_STRCO	P35925	streptomyc	208	6	1.2	261	1	YFGF_ECOLI	P52045	eschlerichia
136	6	1.2	192	1	PAAD_CHLTR	O84222	chlamydia t	209	6	1.2	264	1	CLDI_MOUSE	P56857	mus musculus
137	6	1.2	192	1	SCPA_PENSP	P02636	penaeus sp.	210	6	1.2	264	1	YFLN_BACSU	Q34409	bacillus su
138	6	1.2	192	1	YD37_SCHPO	Q10271	schizosacch	211	6	1.2	265	1	LICD_HAEIN	P14184	haemophilus
139	6	1.2	194	1	GSFH_VIBCH	P45774	vibrio chol	212	6	1.2	266	1	C561_CAEEL	P34465	caenorhabdi
140	6	1.2	195	1	MSA2_RHILLO	Q98dv6	rhizobium l	213	6	1.2	266	1	COX3_MAGGR	Q95840	magnaporthe
141	6	1.2	196	1	MOBA_STACA	Q92im7	staphylococ	214	6	1.2	269	1	TPIS_MORSP	Q01893	moraxella s
142	6	1.2	196	1	TSAL_CANAL	Q9y7f0	candida alb	215	6	1.2	271	1	SRPB_HUMAN	Q9V5m8	homo sapien
143	6	1.2	198	1	MCRC_METTH	O27234	methanobact	216	6	1.2	272	1	ISPA_BACSU	P54383	bacillus su
144	6	1.2	198	1	MCRC_METTM	P11566	methanobact	217	6	1.2	273	1	FLJO_CAUCR	O52531	caulobacter
145	6	1.2	199	1	SECG_HELPJ	Q9Zjx2	helicobacte	218	6	1.2	275	1	SE34_YEAST	P39707	saccharomyc
146	6	1.2	199	1	PDXL_MOUSE	P35700	mus musculus	219	6	1.2	275	1	VGLM_PUUMB	P41264	puumala vir
147	6	1.2	199	1	PDXL_RAT	Q63716	rattus norv	220	6	1.2	278	1	HM37_CAEEL	Q93356	caenorhabdi
148	6	1.2	199	1	SECG_HELPY	O25847	helicobacte	221	6	1.2	279	1	EFTS_BORBU	O51148	borrelia bu
149	6	1.2	199	1	TDX_TRYBR	Q26695	trypanosoma	222	6	1.2	286	1	AACB_STRFR	P29809	streptomyc
150	6	1.2	199	1	YIHX_ECOLI	P32145	eschlerichia	223	6	1.2	286	1	POTC_MYCPN	P75057	mycoplasma
151	6	1.2	200	1	MCRV_METJA	Q58254	methanococc	224	6	1.2	288	1	ISPE_CHLTR	O84810	chlamydia t
152	6	1.2	200	1	TDX_ONCPY	Q90384	cynops pyr	225	6	1.2	289	1	GNPL_HUMAN	P46926	homo sapien
153	6	1.2	200	1	TDX_ONCPY	Q91191	oncorhynch	226	6	1.2	289	1	GNPL_MESAU	Q64422	mesocricetu
154	6	1.2	203	1	NH10_YEAST	O03435	saccharomyc	227	6	1.2	289	1	GNPL_MOUSE	O88958	mus musculus
155	6	1.2	207	1	SODE_MYCTU	P17670	mycobacteri	228	6	1.2	289	1	MYOD_XENLA	P13904	xenopus lae
156	6	1.2	208	1	YSX2_CAEEL	Q10021	caenorhabdi	229	6	1.2	290	1	UL49_HSV4	Q00039	equine herp
157	6	1.2	213	1	HIS5_CAUCR	P9a231	caulobacter	230	6	1.2	291	1	EFTS_UREPA	O9ppx5	ureaplasma
158	6	1.2	215	1	CYB6_OPOSI	P94888	odontella s	231	6	1.2	296	1	NADL_ECOLI	Q35682	mus musculus
159	6	1.2	215	1	CYB6_SKECO	O96801	skeletonema	232	6	1.2	296	1	YAYQ_RHISN	P30011	eschlerichia
160	6	1.2	215	1	Y256_HAEIN	P43973	haemophilus	233	6	1.2	298	1	V884_HSV62	P57253	rhizobium s
161	6	1.2	218	1	UVRY_ECOLI	P07027	eschlerichia	234	6	1.2	300	1	NC5R_RAT	P20070	rattus norv
162	6	1.2	219	1	FLIZ_BACSU	P35536	bacillus su	235	6	1.2	300	1	VP33_APLCA	P30507	agrobacteri
163	6	1.2	222	1	CCG1_RABIT	P19518	oryctolagus	236	6	1.2	300	1	RP32_AGRTR	P49423	prochloroco
164	6	1.2	223	1	IF6_SULAC	P38619	sulfolobus	237	6	1.2	302	1	DAPA_PROMA	Q9pf75	xyliella fas
165	6	1.2	224	1	NEPL_AERPE	Q9yes9	aeropyrum p	238	6	1.2	302	1	LPXC_XYLF	Q34776	synthococc
166	6	1.2	226	1	FLGA_BUCAY	P57418	buchnera ap	239	6	1.2	304	1	ACCD_SYNP7	Q13609	homo sapien
167	6	1.2	226	1	OPBD_BACSU	P39775	bacillus su	240	6	1.2	305	1	DRNG_HUMAN	P06622	pseudomonas
168	6	1.2	227	1	MTR2_MOUSE	Q922d1	mus musculus	241	6	1.2	307	1	YIEL_PSEPU	P72855	synthocyst
169	6	1.2	227	1	Y173_TREPA	O83203	treponema p	242	6	1.2	308	1	Y964_SYNY3	Q55070	mus musculus
170	6	1.2	227	1	Y5E0_ARCFU	O28812	archaeoglob	243	6	1.2	310	1	DRNG_MOUSE	O89107	rattus norv
171	6	1.2	228	1	HS74_LEIMA	P12077	leishmania	244	6	1.2	310	1	LDH_THECA	P06150	thermus cal
172	6	1.2	229	1	OPCD_BACSU	O34742	bacillus su	245	6	1.2	310	1	MIAA_BRUME	O8y129	bruceella me
173	6	1.2	229	1	PRL_CHICK	P14676	gallus gall	246	6	1.2	312	1	FMT_LISIN	Q92a15	listeria in
174	6	1.2	229	1	PRL_MELGA	P17572	meleagris g	247	6	1.2	312	1	FMT_LISIN	Q8y676	listeria mo
175	6	1.2	229	1	RS3_ARCFU	O28360	archaeoglob	248	6	1.2	312	1	GUB2_HORVU	P12257	hordeum vul
176	6	1.2	230	1	NEP_SIVAI	P27970	simian immu	249	6	1.2	316	1	YIW3_YEAST	P05087	saccharomyc
177	6	1.2	230	1	RT07_NARPO	P26867	marichantia	250	6	1.2	317	1	EXOZ_RHIME	P26502	rhizobium m
178	6	1.2	231	1	DLHH_AQUAE	O67802	aquifex aeo	251	6	1.2	317	1	YK88_CAEEL	P46558	caenorhabdi
179	6	1.2	231	1	NU4M_BOTLA	O03700	bothriechlis	252	6	1.2	317	1	YK88_CAEEL	P46558	caenorhabdi

253	6	1.2	317	1	YRP2_CABEL	Q09344	caenorhabdi	326	1	BRB2_RABIT	Q28642	oryctolagus
254	6	1.2	318	1	NRF2_ECOLI	P32709	escherichia	327	1	CCR3_MOUSE	O88410	mus musculus
255	6	1.2	319	1	RTBP_ADE03	P04501	human adeno	328	1	CCR3_HUMAN	P49682	homo sapien
256	6	1.2	320	1	PSTC_MYCLE	O50098	mycobacteri	329	1	GALT_HUMAN	O60755	homo sapien
257	6	1.2	321	1	YOJP_BACSU	P54553	bacillus su	330	1	ILVE_MYCTU	O32954	mycobacteri
258	6	1.2	322	1	MYDM_ENTHR	O07668	enterococcu	331	1	ILVE_MYCTU	O10399	mycobacteri
259	6	1.2	323	1	MYDM_HUMAN	O07668	enterococcu	332	1	ILVE_MYCTU	O10399	mycobacteri
260	6	1.2	324	1	PREA_PORPU	P51272	paracentrot	333	1	GALT_MOUSE	O88853	mus musculus
261	6	1.2	325	1	YU70_YEAST	P12772	paracentrot	334	1	GALT_MOUSE	O88626	rattus norv
262	6	1.2	326	1	BTUC_ECOLI	O10685	mycobacteri	335	1	GALT_MOUSE	O88854	mus musculus
263	6	1.2	327	1	BTUC_ECOLI	O8x417	escherichia	336	1	GALT_MOUSE	O70526	cavia porce
264	6	1.2	328	1	BTUC_SALTI	O06609	escherichia	337	1	GALT_MOUSE	O08726	rattus norv
265	6	1.2	329	1	FCN1_HUMAN	Q82615	salmonella	338	1	GALT_MOUSE	O11203	homo sapien
266	6	1.2	330	1	FCN1_HUMAN	O00602	homo sapien	339	1	GALT_MOUSE	O06587	homo sapien
267	6	1.2	331	1	FCN1_HUMAN	P14061	homo sapien	340	1	GALT_MOUSE	O99500	homo sapien
268	6	1.2	332	1	FCN1_HUMAN	P28304	escherichia	341	1	GALT_MOUSE	O61492	drosophila
269	6	1.2	333	1	FCN1_HUMAN	Q29298	chlamydia p	342	1	GALT_MOUSE	P48886	felis silve
270	6	1.2	334	1	FCN1_HUMAN	Q04866	salmonella	343	1	GALT_MOUSE	O35655	panthera ti
271	6	1.2	335	1	FCN1_HUMAN	P47140	saccharomyc	344	1	GALT_MOUSE	P07902	homo sapien
272	6	1.2	336	1	FCN1_HUMAN	Q95011	homo sapien	345	1	GALT_MOUSE	P43424	rattus norv
273	6	1.2	337	1	FCN1_HUMAN	Q9a095	streptococc	346	1	GALT_MOUSE	O14408	metarhizium
274	6	1.2	338	1	FCN1_HUMAN	Q9ch70	lactococcus	347	1	GALT_MOUSE	P80370	homo sapien
275	6	1.2	339	1	FCN1_HUMAN	Q06844	halobacteri	348	1	GALT_MOUSE	P32515	equine herp
276	6	1.2	340	1	FCN1_HUMAN	P14491	staphylococ	349	1	GALT_MOUSE	P17583	escherichia
277	6	1.2	341	1	FCN1_HUMAN	Q9x1m5	thermotoga	350	1	GALT_MOUSE	P48667	homo sapien
278	6	1.2	342	1	FCN1_HUMAN	P28523	zea mays (m	351	1	GALT_MOUSE	P79393	bos taurus
279	6	1.2	343	1	FCN1_HUMAN	O13802	schizosacch	352	1	GALT_MOUSE	P33361	escherichia
280	6	1.2	344	1	FCN1_HUMAN	Q9w9f7	myxoma viru	353	1	GALT_MOUSE	P58335	homo sapien
281	6	1.2	345	1	FCN1_HUMAN	P57907	pasteurella	354	1	GALT_MOUSE	P43119	homo sapien
282	6	1.2	346	1	FCN1_HUMAN	Q9w963	thermotoga	355	1	GALT_MOUSE	O43603	homo sapien
283	6	1.2	347	1	FCN1_HUMAN	O84762	chlamydia t	356	1	GALT_MOUSE	Q921y6	cavia porce
284	6	1.2	348	1	FCN1_HUMAN	P77795	escherichia	357	1	GALT_MOUSE	P09533	cercopithec
285	6	1.2	349	1	FCN1_HUMAN	Q9i267	delnoccoccu	358	1	GALT_MOUSE	O19011	equus caball
286	6	1.2	350	1	FCN1_HUMAN	Q90262	brachydanio	359	1	GALT_MOUSE	P01137	homo sapien
287	6	1.2	351	1	FCN1_HUMAN	Q55025	synecococc	360	1	GALT_MOUSE	P07200	sus scrofa
288	6	1.2	352	1	FCN1_HUMAN	Q8uiv7	agrobacteri	361	1	GALT_MOUSE	Q08298	arabidopsis
289	6	1.2	353	1	FCN1_HUMAN	O02056	caenorhabdi	362	1	GALT_MOUSE	O22915	caenorhabdi
290	6	1.2	354	1	FCN1_HUMAN	P47936	mus musculus	363	1	GALT_MOUSE	Q55147	synecocyst
291	6	1.2	355	1	FCN1_HUMAN	O71027	african hor	364	1	GALT_MOUSE	Q44482	anabaena va
292	6	1.2	356	1	FCN1_HUMAN	Q86729	african hor	365	1	GALT_MOUSE	P10551	saccharomyc
293	6	1.2	357	1	FCN1_HUMAN	P36325	african hor	366	1	GALT_MOUSE	P41338	saccharomyc
294	6	1.2	358	1	FCN1_HUMAN	Q9fh88	arabidopsis	367	1	GALT_MOUSE	P57312	buchnera ap
295	6	1.2	359	1	FCN1_HUMAN	Q28690	oryctolagus	368	1	GALT_MOUSE	Q9h1y3	homo sapien
296	6	1.2	360	1	FCN1_HUMAN	P52205	bos taurus	369	1	GALT_MOUSE	P04278	homo sapien
297	6	1.2	361	1	FCN1_HUMAN	P13370	drosophila	370	1	GALT_MOUSE	O95f40	arabidopsis
298	6	1.2	362	1	FCN1_HUMAN	Q02334	caenorhabdi	371	1	GALT_MOUSE	P49691	arabidopsis
299	6	1.2	363	1	FCN1_HUMAN	Q42899	lotus japon	372	1	GALT_MOUSE	P09180	drosophila
300	6	1.2	364	1	FCN1_HUMAN	P04078	medicago sa	373	1	GALT_MOUSE	Q9xf97	prunus arme
301	6	1.2	365	1	FCN1_HUMAN	P04770	phaseolus v	374	1	GALT_MOUSE	P31428	mus musculus
302	6	1.2	366	1	FCN1_HUMAN	P51118	vitis vinif	375	1	GALT_MOUSE	P31430	rattus norv
303	6	1.2	367	1	FCN1_HUMAN	O82560	glycine max	376	1	GALT_MOUSE	P42784	synecococc
304	6	1.2	368	1	FCN1_HUMAN	P00965	phaseolus v	377	1	GALT_MOUSE	P39435	escherichia
305	6	1.2	369	1	FCN1_HUMAN	P32289	vigna acon	378	1	GALT_MOUSE	Q9w315	drosophila
306	6	1.2	370	1	FCN1_HUMAN	P52179	pinus sylve	379	1	GALT_MOUSE	P16457	escherichia
307	6	1.2	371	1	FCN1_HUMAN	P32783	saccharomyc	380	1	GALT_MOUSE	P04047	bacillus su
308	6	1.2	372	1	FCN1_HUMAN	P31302	ustilago ma	381	1	GALT_MOUSE	P22711	drosophila
309	6	1.2	373	1	FCN1_HUMAN	P03192	epstein-bar	382	1	GALT_MOUSE	Q9y9j2	aeropyrum p
310	6	1.2	374	1	FCN1_HUMAN	O16294	caenorhabdi	383	1	GALT_MOUSE	P22711	drosophila
311	6	1.2	375	1	FCN1_HUMAN	Q9zft5	bacillus an	384	1	GALT_MOUSE	Q94123	agarius bi
312	6	1.2	376	1	FCN1_HUMAN	P21137	caenorhabdi	385	1	GALT_MOUSE	O51530	oxalobacter
313	6	1.2	377	1	FCN1_HUMAN	Q99063	ustilago ho	386	1	GALT_MOUSE	O86053	meiothermus
314	6	1.2	378	1	FCN1_HUMAN	P34972	homo sapien	387	1	GALT_MOUSE	Q9sd33	arabidopsis
315	6	1.2	379	1	FCN1_HUMAN	Q9kpg4	vibrio chol	388	1	GALT_MOUSE	O82y67	pyrobaculum
316	6	1.2	380	1	FCN1_HUMAN	P04672	glycine max	389	1	GALT_MOUSE	O9f414	mycobacteri
317	6	1.2	381	1	FCN1_HUMAN	P42806	pseudomonas	390	1	GALT_MOUSE	Q9d8e6	mus musculus
318	6	1.2	382	1	FCN1_HUMAN	Q9xyn0	schistocerc	391	1	GALT_MOUSE	O28346	canis fami
319	6	1.2	383	1	FCN1_HUMAN	P19112	rattus norv	392	1	GALT_MOUSE	P50878	rattus norv
320	6	1.2	384	1	FCN1_HUMAN	P27716	drosophila	393	1	GALT_MOUSE	Q9p5s2	schizosacch
321	6	1.2	385	1	FCN1_HUMAN	Q60342	methanococc	394	1	GALT_MOUSE	P04962	spisula sol
322	6	1.2	386	1	FCN1_HUMAN	P07373	bacillus su	395	1	GALT_MOUSE	P08819	trititum ae
323	6	1.2	387	1	FCN1_HUMAN	Q9g1x8	sus scrofa	396	1	GALT_MOUSE	P16770	human cytom
324	6	1.2	388	1	FCN1_HUMAN			397	1	GALT_MOUSE	P33608	escherichia
325	6	1.2	389	1	FCN1_HUMAN			398	1	GALT_MOUSE	O75038	homo sapien

399	6	1.2	426	1	CGED_BACSU	P42092	Bacillus su	472	6	1.2	481	1	MM20_BOVIN	O18767	bos taurus
400	6	1.2	426	1	MNTH_MYCLE	Q50103	mycobacteri	473	6	1.2	483	1	MM20_PIG	P79287	sus scrofa
401	6	1.2	426	1	STE2_SACKL	P12384	saccharomyc	474	6	1.2	485	1	ER24_FUSSO	Q01447	fusarium so
402	6	1.2	427	1	RL4_HUMAN	P36578	homo sapien	475	6	1.2	485	1	MAIQ_AQUAE	P69937	aquifex aeo
403	6	1.2	428	1	GGPP_NEUCR	P24322	n geranylge	476	6	1.2	485	1	YIHO_ECOLI	P32136	escherichia
404	6	1.2	428	1	YFUD_ECOLI	P37908	escherichia	477	6	1.2	488	1	FLID_XENNE	P06927	xenorhabdus
405	6	1.2	429	1	ENO_ANASP	Q8YrB0	anabaena sp	478	6	1.2	488	1	NU4M_ASPAM	P03913	aspergillus
406	6	1.2	430	1	GLN2_ARATH	Q43127	arabidopsis	479	6	1.2	489	1	MDM2_MOUSE	P23804	mus musculus
407	6	1.2	432	1	GLXA_BRAJA	P24060	bradyrhizob	480	6	1.2	489	1	YHIP_ECOLI	P36837	escherichia
408	6	1.2	433	1	CITM_BACSU	P55069	Bacillus su	481	6	1.2	490	1	LIPL_CHICK	P11602	gallus gall
409	6	1.2	433	1	LGMN_HUMAN	Q99538	homo sapien	482	6	1.2	494	1	CYSN_RHTR	O33581	rhizobium t
410	6	1.2	433	1	TCR_STRAU	P02983	staphylococ	483	6	1.2	494	1	HEM2_ORYSA	O22101	oryza sativ
411	6	1.2	435	1	LGMN_MOUSE	O89017	mus musculu	484	6	1.2	494	1	LIPL_RAT	P07867	rattus norv
412	6	1.2	435	1	LGMN_RAT	Q91018	rattus norv	485	6	1.2	494	1	SYE_STRCO	O86528	streptomyce
413	6	1.2	435	1	ORCS_HUMAN	Q43913	homo sapien	486	6	1.2	495	1	CD5_BOVIN	P19238	bos taurus
414	6	1.2	435	1	ORCS_MOUSE	Q9WUV0	mus musculu	487	6	1.2	495	1	ENP2_MOUSE	O55026	mus musculus
415	6	1.2	437	1	HEM1_ARCFU	O28304	archaeoglob	488	6	1.2	497	1	KPYC_ARATH	O65595	arabidopsis
416	6	1.2	438	1	FAS5_RHOFA	P46377	rhodococcus	489	6	1.2	497	1	SR51_HORVU	P49968	hordeum vul
417	6	1.2	438	1	MAT2_PSEAE	Q9RPF2	pseudomonas	490	6	1.2	497	1	SR52_HORVU	P49969	hordeum vul
418	6	1.2	439	1	MATK_EPTVI	P30071	epifagus vi	491	6	1.2	498	1	YOKI_CABEL	Q09285	caenorhabdi
419	6	1.2	439	1	SECY_SYNPF	P31159	synecococc	492	6	1.2	498	1	CYSN_RHIME	P56893	rhizobium m
420	6	1.2	440	1	SCAL_DRONE	P30052	drosohilla	493	6	1.2	499	1	GAK_MOUSE	O99K44	mus musculus
421	6	1.2	441	1	DIHR_ACHDO	P16983	acheta dome	494	6	1.2	500	1	LIPL_HUMAN	P11150	homo sapien
422	6	1.2	441	1	HS7C_CABER	P19208	caenorhabdi	495	6	1.2	500	1	C912_ARATH	O65790	arabidopsis
423	6	1.2	441	1	YBE6_YEAST	P38193	saccharomyc	496	6	1.2	502	1	C340_ORYLA	Q98491	oryzias lat
424	6	1.2	442	1	XJBI_ECOLI	P32690	escherichia	497	6	1.2	502	1	Y190_HELPJ	Q92mp2	helicobacte
425	6	1.2	444	1	GAT6_MOUSE	Q61169	mus musculu	498	6	1.2	502	1	Y190_HELPJ	P56117	helicobacte
426	6	1.2	445	1	CANA_CANEN	P50477	canavalia e	499	6	1.2	503	1	CP3H_CAVPO	Q64409	cavia porce
427	6	1.2	445	1	CANA_CANGL	P10562	canavalia g	500	6	1.2	503	1	HS70_PENCI	Q92260	penicillium
428	6	1.2	445	1	YHFM_ECOLI	P45539	escherichia	501	6	1.2	503	1	Y2N3_YEAST	P53832	saccharomyc
429	6	1.2	447	1	G21A_DRONE	Q9VET1	drosohilla	502	6	1.2	505	1	ATPA_ANTSP	Q02848	antithamnio
430	6	1.2	447	1	NAPE_ENTFA	P37062	enterococcu	503	6	1.2	507	1	MOSB_RHIME	Q73608	rhizobium m
431	6	1.2	448	1	Y260_TREPA	O83284	treponema p	504	6	1.2	512	1	C4D1_DRONE	P33269	drosohilla
432	6	1.2	449	1	MURD_STRAM	Q33595	staphylococ	505	6	1.2	512	1	C4D1_DRONE	P33269	drosohilla
433	6	1.2	449	1	STRK_STRGR	P09401	streptomyce	506	6	1.2	512	1	GUAA_CHLMO	O16805	drosohilla
434	6	1.2	452	1	YP59_MYCTU	O50739	mycobacteri	507	6	1.2	512	1	K2C5_XENLA	Q9PKM3	chlamydia m
435	6	1.2	454	1	MNTH_RHITO	O98199	rhizobium l	508	6	1.2	512	1	VC02_VACCV	P16878	xenopus lae
436	6	1.2	456	1	YC88_MYCTU	O10614	mycobacteri	509	6	1.2	516	1	HS70_LEIMA	P17371	vaccinia vi
437	6	1.2	459	1	TCR2_BACSU	P14512	Bacillus su	510	6	1.2	519	1	CP5V_CANAP	P14834	leishmania
438	6	1.2	459	1	YJME_BACSU	Q34961	Bacillus su	511	6	1.2	519	1	DPVS_MOUSE	Q9eqf5	mus musculus
439	6	1.2	461	1	DCUC_ECOLI	Q47134	escherichia	512	6	1.2	521	1	GLG3_ARATH	O63150	rattus norv
440	6	1.2	461	1	US45_LACLC	P22865	lactococcus	513	6	1.2	521	1	MCS4_SCHPO	P55231	arabidopsis
441	6	1.2	462	1	PRTF_ERWCH	P23598	erwinia chr	514	6	1.2	522	1	NU62_HUMAN	P87323	schizosacch
442	6	1.2	462	1	REGB_RHOSH	Q53068	rhodobacter	515	6	1.2	522	1	GLG4_ARATH	P37198	homo sapien
443	6	1.2	462	1	TRPE_LEPBI	P20463	leptospira	516	6	1.2	523	1	ASPA_CORGL	O961k1	arabidopsis
444	6	1.2	463	1	Y096_MYCTU	O10892	mycobacteri	517	6	1.2	526	1	CH62_CHLPN	Q59200	corynebacte
445	6	1.2	465	1	ALST_BACSU	Q45068	Bacillus su	518	6	1.2	526	1	DNB2_ADE02	Q927c9	chlamydia p
446	6	1.2	465	1	LIPL_BOVIN	P11151	bos taurus	519	6	1.2	529	1	DNB2_ADE02	P03264	human adeno
447	6	1.2	465	1	LIPL_CAVPO	P11153	cavia porce	520	6	1.2	529	1	YGA_A_ECOLI	P03265	human adeno
448	6	1.2	465	1	MM12_RAT	O63341	rattus norv	521	6	1.2	532	1	FM05_CAVPO	P37013	escherichia
449	6	1.2	468	1	KG3H_DICDI	P51136	dictyosteli	522	6	1.2	532	1	P72_MYCHY	P49109	cavia porce
450	6	1.2	468	1	K1CX_HUMAN	Q56228	thermus the	523	6	1.2	532	1	SKIP_HUMAN	P43326	homo sapien
451	6	1.2	469	1	NOOD_THETH	P08779	homo sapien	524	6	1.2	532	1	SKIP_HUMAN	P22698	dictyosteli
452	6	1.2	469	1	SECY_SULSO	Q9UX84	Sulfolobus su	525	6	1.2	536	1	PIRG_CHLPN	Q13573	homo sapien
453	6	1.2	470	1	ROCC_BACSU	P39636	Bacillus su	526	6	1.2	537	1	TYR1_MOUSE	Q928u8	chlamydia p
454	6	1.2	470	1	YMP8_CABEL	P53993	caenorhabdi	527	6	1.2	537	1	IF3C_EUGGR	P07147	mus musculus
455	6	1.2	471	1	K1CN_HUMAN	P02533	homo sapien	528	6	1.2	538	1	SGLT_VIBPA	P36177	euglena gra
456	6	1.2	471	1	RBL2_HYDMR	Q59460	hydrogenovi	529	6	1.2	538	1	CLL1_SOLTU	P96169	vibrio para
457	6	1.2	473	1	K1CP_HUMAN	P50654	homo sapien	530	6	1.2	543	1	CLL2_SOLTU	Q43068	pisum sativ
458	6	1.2	474	1	LIPL_MOUSE	P11152	mus musculu	531	6	1.2	544	1	CLL1_PEA	P31685	solanum tub
459	6	1.2	474	1	LIPL_RAT	Q06000	rattus norv	532	6	1.2	545	1	CH60_PSEPU	P48216	pseudomonas
460	6	1.2	475	1	LIPL_HUMAN	O46647	mustela vis	533	6	1.2	545	1	4CL1_TOBAC	P51852	azospirillum
461	6	1.2	475	1	LIPL_MOUSE	Q926v8	chlamydia p	534	6	1.2	545	1	LIPL2_CANRU	O24145	nicotiana t
462	6	1.2	475	1	LIPL_PAPAN	P49060	papio anubi	535	6	1.2	547	1	FAST_HUMAN	P32946	candida rug
463	6	1.2	476	1	GLGA_CHLPN	P76658	escherichia	536	6	1.2	548	1	LIPL3_CANRU	Q14296	homo sapien
464	6	1.2	477	1	REAE_ECOLI	P42590	escherichia	537	6	1.2	549	1	LIPL4_CANRU	P32947	candida rug
465	6	1.2	477	1	YGIU_ECOLI	P31593	nicotiana t	538	6	1.2	549	1	LIPL5_CANRU	P32948	candida rug
466	6	1.2	478	1	GSA_TOBAC	P55031	felis silve	539	6	1.2	549	1	LIPL_SHEEP	P40877	escherichia
467	6	1.2	478	1	LIPL_FELCA	Q99524	ovis aries	540	6	1.2	550	1	IL2B_HUMAN	P14784	homo sapien
468	6	1.2	478	1	LIPL_PIG	P96335	haemophilus	541	6	1.2	551	1	HMEN_DRONE	P02836	drosohilla
469	6	1.2	478	1	LIPL_SHEEP			542	6	1.2	552	1			
470	6	1.2	480	1	GLPT_HAEIN			543	6	1.2					
471	6	1.2	481	1	KRI_HSV11			544	6	1.2					

545	6	1.2	552	1	K2C6_MOUSE	P50446	mus musculus	618	1.2	610	1	DNAK_STAAU	P45554	staphylococ
546	6	1.2	552	1	YM81_MYCTU	Q50684	mycobacteri	619	1.2	611	1	ADAS_DICTDI	Q96759	dityostel
547	6	1.2	554	1	SERA_SYNY3	P73821	synecocyst	620	6	611	1	BACHE_RHOSH	Q9rfd3	rickettsia
548	6	1.2	555	1	DP87_DICTDI	Q04503	dictyostell	621	6	611	1	HSCA_BUCAI	P57660	buchnera ap
549	6	1.2	556	1	HSCC_ECOLI	P77319	escherichia	622	6	612	1	DNAK_LISIN	Q92bn8	listeria in
550	6	1.2	557	1	MCP5_ENTAE	P21822	enterobacte	623	6	612	1	DNAK_LISMO	Q95544	listeria mo
551	6	1.2	557	1	FLIF_SALTY	P15928	salmoneilla	624	6	612	1	HS75_KLUMA	P41770	kluveromye
552	6	1.2	558	1	K2CA_HUMAN	P02538	homo sapien	625	6	612	1	HS75_YEAST	P40150	saccharomyc
553	6	1.2	563	1	K2CB_HUMAN	P04259	homo sapien	626	6	612	1	PLB1_PENCH	P39457	penicillium
554	6	1.2	563	1	K2CC_HUMAN	P48666	homo sapien	627	6	612	1	DNAK_BACHD	Q9kd72	bacillus ha
555	6	1.2	563	1	K2CE_HUMAN	P48668	homo sapien	628	6	613	1	DNAK_LAGSK	O87777	lactobacill
556	6	1.2	563	1	D2CF_HUMAN	P48669	homo sapien	629	6	613	1	HS75_CANAL	P87222	candida alb
557	6	1.2	565	1	DSBD_ECO57	P58162	escherichia	630	6	613	1	HS75_SCHPO	Q10284	schizosacch
558	6	1.2	565	1	DSBD_ECOLI	P36655	escherichia	631	6	614	1	DNAK_CLOAB	P30721	clostridium
559	6	1.2	567	1	DSBD_SALTI	O8zla8	salmoneilla	632	6	614	1	DNAK_ODOSI	P49463	odontella s
560	6	1.2	567	1	DSBD_SALTY	O8zxc3	salmoneilla	633	6	614	1	DNAK_DROME	P48602	drosophila
561	6	1.2	568	1	FLG_ZYGBI	P13784	zygosacchar	634	6	614	1	VAA1_DROME	P48602	drosophila
562	6	1.2	571	1	UGM4_YEAST	P32837	saccharomyc	635	6	614	1	VAA2_DROME	Q27331	drosophila
563	6	1.2	573	1	C114_MOUSE	P19467	mus musculus	636	6	615	1	DNAK_THETH	Q26235	thermus the
564	6	1.2	573	1	SECD_MYCTU	Q50634	mycobacteri	637	6	615	1	VATA_AEDAE	O16109	aedes aegypt
565	6	1.2	574	1	SPKB_SYNY3	P74297	synecocyst	638	6	616	1	HSCA_ECOLI	P36541	escherichia
566	6	1.2	575	1	COLL_DROME	P56721	drosophila	639	6	616	1	TR11_HUMAN	Q9y6q6	homo sapien
567	6	1.2	575	1	FUT8_MOUSE	Q9wts2	m alpha-(1,	640	6	617	1	DNAK_PROAC	Q917p1	propionibac
568	6	1.2	575	1	ML1X_SHEEP	Q28558	ovis aries	641	6	617	1	MBHL_ALCEU	P31891	alcaligenes
569	6	1.2	578	1	YDEM_CABEL	O19124	caenorhabdi	642	6	618	1	DNAK_CYACA	Q9tlt1	cyandium c
570	6	1.2	578	1	YDV8_SCHPO	O14226	schizosacch	643	6	618	1	DNAK_DEIPR	P46955	deinococcus
571	6	1.2	579	1	SYD_THEMEA	Q9xl14	thermotoga	644	6	618	1	DNAK_STRCO	Q05558	streptomyce
572	6	1.2	581	1	PGMU_BROIN	Q9gnx2	bromus iner	645	6	618	1	DNAK_STRGE	Q54215	streptomyce
573	6	1.2	583	1	PMEU_LYCES	Q43143	lycopersico	646	6	619	1	DNAK_HELPJ	P26823	clostridium
574	6	1.2	585	1	MECR_STAAM	P26597	staphylococ	647	6	619	1	DNAK_HELPJ	Q9zmw4	helicobacte
575	6	1.2	587	1	HE_PARLI	P22757	paracentrot	648	6	619	1	DNAK_METPA	P55994	helicobacte
576	6	1.2	588	1	SYD_HAETN	P43817	haemophilus	649	6	619	1	DNAK_METMA	P27094	methanosarc
577	6	1.2	588	1	SYD_PASMU	P57895	pasteurella	650	6	619	1	DNAK_MYCLE	P19593	mycobacteri
578	6	1.2	589	1	SYFE_DROME	Q9vca5	drosophila	651	6	619	1	HSCA_HAETN	P44669	haemophilus
579	6	1.2	590	1	DNAK_MYCCA	Q8z5w1	salmoneilla	652	6	619	1	HSCA_PSEAE	Q51382	pseudomonas
580	6	1.2	590	1	BETP_CONGL	Q9zdw5	rickettsia	653	6	620	1	DNAK_PORPU	P30723	porphyra pu
581	6	1.2	590	1	DNAK_MYCCE	P47547	mycoplasma	654	6	620	1	NODQ_AZOBR	P28604	a nodq bifu
582	6	1.2	590	1	DNAK_MYCHO	Q9zejo	mycoplasma	655	6	621	1	MBHL_ALCHY	P33374	alcaligenes
583	6	1.2	590	1	DNAK_MYCPN	Q9zdw5	rickettsia	656	6	622	1	DNAK_MYCPA	Q00488	mycobacteri
584	6	1.2	591	1	DNAK_MYCPN	P47547	mycoplasma	657	6	622	1	DNAK_MYCPA	Q00488	mycobacteri
585	6	1.2	593	1	HSCA_RICPR	Q9zdw5	rickettsia	658	6	623	1	DNAK_CAMJE	Q69298	campylobact
586	6	1.2	595	1	DNAK_MYCCE	P47547	mycoplasma	659	6	623	1	DNAK_CAMJE	Q69298	campylobact
587	6	1.2	595	1	DNAK_MYCCE	P47547	mycoplasma	660	6	623	1	DNAK_CAMJE	Q69298	campylobact
588	6	1.2	595	1	DNAK_MYCCE	P47547	mycoplasma	661	6	623	1	DNAK_CAMJE	Q69298	campylobact
589	6	1.2	595	1	DNAK_MYCCE	P47547	mycoplasma	662	6	623	1	DNAK_CAMJE	Q69298	campylobact
590	6	1.2	596	1	DNAK_THEMEA	Q9ywk6	thermotoga	663	6	627	1	DNAK_RICCN	Q37106	cyanophora
591	6	1.2	596	1	MBHL_BRAJA	P12636	bradyrhizob	664	6	624	1	DNAK_MYCTU	Q37223	mycobacteri
592	6	1.2	596	1	MBHL_RHILV	P18636	rhizobium l	665	6	624	1	DNAK_MYCTU	Q37223	mycobacteri
593	6	1.2	599	1	ABEL_HUMAN	Q96b10	homo sapien	666	6	625	1	DUS8_HALME	Q9hb9	halobacteri
594	6	1.2	599	1	DNAK_MYCPO	Q98qy7	mycoplasma	667	6	625	1	DNAK_HALME	Q9hb9	halobacteri
595	6	1.2	599	1	HS7S_SPTOL	Q08080	spinacia ol	668	6	625	1	DNAK_HALME	Q9hb9	halobacteri
596	6	1.2	600	1	DNAK_ERYEH	Q05647	erysipeloth	669	6	625	1	DNAK_HALME	Q9hb9	halobacteri
597	6	1.2	600	1	DNAK_MYCHY	Q95939	mycoplasma	670	6	625	1	DNAK_HALME	Q9hb9	halobacteri
598	6	1.2	600	1	ESR1_RAT	P06211	rattus norv	671	6	625	1	DNAK_HALME	Q9hb9	halobacteri
599	6	1.2	602	1	MBHL_AZOV1	P21949	azotobacter	672	6	625	1	DNAK_HALME	Q9hb9	halobacteri
600	6	1.2	602	1	SYD_RICCN	Q92j82	rickettsia	673	6	625	1	DNAK_HALME	Q9hb9	halobacteri
601	6	1.2	603	1	DNAK_UREPA	Q9pqf2	ureaplasma	674	6	627	1	DNAK_GUITH	Q92j36	rickettsia
602	6	1.2	604	1	DNAK_BACNE	P05646	bacillus me	675	6	627	1	DNAK_GUITH	Q92j36	rickettsia
603	6	1.2	605	1	APM2_YEAST	P38700	saccharomyc	676	6	627	1	DNAK_GUITH	Q92j36	rickettsia
604	6	1.2	605	1	SL51_PIG	P26429	sus scrofa	677	6	627	1	DNAK_GUITH	Q92j36	rickettsia
605	6	1.2	606	1	DNAK_BACTR	Q9kws7	bacillus th	678	6	627	1	DNAK_GUITH	Q92j36	rickettsia
606	6	1.2	606	1	KINA_BACSU	P16497	bacillus su	679	6	627	1	DNAK_GUITH	Q92j36	rickettsia
607	6	1.2	607	1	DNAK_BACST	Q45551	bacillus st	680	6	627	1	DNAK_GUITH	Q92j36	rickettsia
608	6	1.2	607	1	DNAK_LACLA	P42368	lactococcus	681	6	627	1	DNAK_GUITH	Q92j36	rickettsia
609	6	1.2	607	1	DNAK_MYXHA	P95334	myxococcus	682	6	627	1	DNAK_GUITH	Q92j36	rickettsia
610	6	1.2	607	1	DNAK_MYXHA	P95334	myxococcus	683	6	627	1	DNAK_GUITH	Q92j36	rickettsia
611	6	1.2	607	1	DNAK_STRYP	P95831	streptococc	684	6	627	1	DNAK_GUITH	Q92j36	rickettsia
612	6	1.2	608	1	HSCA_BUCAI	O51883	buchnera ap	685	6	627	1	DNAK_GUITH	Q92j36	rickettsia
613	6	1.2	609	1	DNAK_STRAG	P95693	streptococc	686	6	627	1	DNAK_GUITH	Q92j36	rickettsia
614	6	1.2	610	1	DNAK_BACSH	O62688	bacillus sp	687	6	627	1	DNAK_GUITH	Q92j36	rickettsia
615	6	1.2	610	1	DNAK_BACSU	P17820	bacillus su	688	6	627	1	DNAK_GUITH	Q92j36	rickettsia
616	6	1.2	610	1	DNAK_METTE	Q9uxr0	methanosarc	689	6	627	1	DNAK_GUITH	Q92j36	rickettsia
617	6	1.2	610	1	DNAK_STAAM	Q99lr7	staphylococ	690	6	627	1	DNAK_GUITH	Q92j36	rickettsia

691	1	1.2	636	1	DNAX_EHRSE	085282 ehrlichia s	764	1	1.2	645	1	HS70_SOYBN	P26413 glycine max
692	1	1.2	636	1	DNAX_YERPE	Q8zim7 yersinia pe	765	1	1.2	645	1	SUBB_BACSU	P16396 bacillus su
693	1	1.2	636	1	DNK2_SYNY3	P22358 synechocyst	766	1	1.2	645	1	VP74_NPVAC	P15963 autographa
694	1	1.2	637	1	DNAX_BRUME	Q8ve76 brucella me	767	1	1.2	646	1	HS70_NEUCR	Q01233 neurospora
695	1	1.2	637	1	DNAX_BRUCV	Q05981 brucella ov	768	1	1.2	646	1	HS70_THEAN	P16019 theileria a
696	1	1.2	637	1	DNAX_BUCAT	Q32464 buchnera ap	769	1	1.2	646	1	HS7C_CRIGR	P19378 cricetus
697	1	1.2	637	1	DNAX_ECCLI	P04475 escherichia	770	1	1.2	646	1	HS7C_HUMAN	P11142 homo sapien
698	1	1.2	637	1	DNAX_PSEAE	Q9h473 pseudomonas	771	1	1.2	646	1	HS7C_MOUSE	P08109 mus musculus
699	1	1.2	637	1	DNAX_RHOCA	Q52701 rhodobacter	772	1	1.2	647	1	CCME_ECCLI	P33927 escherichia
700	1	1.2	637	1	DNAX_SALTI	Q829r1 salmonella	773	1	1.2	647	1	HS70_XENLA	P02827 xenopus lae
701	1	1.2	637	1	DNAX_SALTY	Q56073 salmonella	774	1	1.2	647	1	VEI_HPV52	P36730 human papil
702	1	1.2	637	1	DNAX_VIBER	Q917r1 vibrio prot	775	1	1.2	647	1	YIK1_YEAST	P40489 saccharomyc
703	1	1.2	637	1	HS70_SCHWA	P08418 schistosoma	776	1	1.2	648	1	HS71_PUCGR	Q01877 puccinia gr
704	1	1.2	638	1	DNAX_PRELO	Q93gfl prevotella	777	1	1.2	648	1	WHN_HUMAN	O15353 homo sapien
705	1	1.2	638	1	DNAX_PSEEG	Q9w9g9 pseudomonas	778	1	1.2	649	1	HS70_BLAEM	P48720 blastocladia
706	1	1.2	638	1	DNAX_RHILE	Q33528 rhizobium l	779	1	1.2	649	1	HS70_CHLRE	P25840 chlamydomon
707	1	1.2	638	1	DNAX_RHILO	Q98dd1 rhizobium l	780	1	1.2	649	1	HS70_PARRB	P87047 paracoccidi
708	1	1.2	638	1	DNAX_XYLFA	Q9pb05 xyella fas	781	1	1.2	649	1	HS73_ARATH	P37899 pyrenomonas
709	1	1.2	638	1	HS70_CERCA	P51902 cercaritis c	782	1	1.2	649	1	HS73_YEAST	O65719 arabidopsis
710	1	1.2	638	1	HS71_CERAE	Q28222 ceratopithe	783	1	1.2	649	1	HS73_YEAST	P09435 saccharomyc
711	1	1.2	638	1	HS72_YEAST	P10592 saccharomyc	784	1	1.2	649	1	HS7C_ICTPU	P47773 ictalurus p
712	1	1.2	639	1	HS71_ORYLA	Q918f9 oryzias lat	785	1	1.2	649	1	PLB1_TORDE	Q11121 torulaspore
713	1	1.2	639	1	HS72_HUMAN	P54652 homo sapien	786	1	1.2	650	1	DNAX_BURCE	P42373 burkholderi
714	1	1.2	639	1	HS74_PARLI	Q06248 paracentrot	787	1	1.2	650	1	DNAX_BURPS	O68191 burkholderi
715	1	1.2	639	1	MET7_YEAST	P47164 saccharomyc	788	1	1.2	650	1	HS7C_BOVIN	P24629 lycopersico
716	1	1.2	639	1	V70K_PLRVM	P11622 potato leaf	789	1	1.2	651	1	HS70_OCNVY	P19120 bos taurus
717	1	1.2	640	1	DNAX_PORGI	Q92ad3 porphyromon	790	1	1.2	651	1	HS7C_OCNVY	P08108 oncorhynch
718	1	1.2	640	1	DNAX_RHOMR	Q9xch1 rhodothermu	791	1	1.2	651	1	HS71_ARATH	P22953 arabidopsis
719	1	1.2	640	1	DNAX_VIBHA	O87384 vibrio harv	792	1	1.2	651	1	HS7C_PETHY	P09189 penultima hyb
720	1	1.2	640	1	HS71_ANOAL	P41825 anopheles a	793	1	1.2	652	1	HS7D_DROME	P11147 drosophila
721	1	1.2	640	1	HS72_ANOAL	P41826 anopheles a	794	1	1.2	652	1	CD93_HUMAN	Q9np53 homo sapien
722	1	1.2	640	1	HS74_ANOAL	P41827 anopheles a	795	1	1.2	652	1	GR78_CHICK	Q90593 gallus gall
723	1	1.2	640	1	HS7A_CAEEL	P09446 caenorhabdi	796	1	1.2	652	1	HS70_ACHKL	P41753 achlya kieb
724	1	1.2	640	1	HS7C_DICDI	P36415 dictyosteli	797	1	1.2	652	1	HS70_LEIAM	Q07437 leishmania
725	1	1.2	641	1	DNAX_METPS	Q9zfc6 methylovoru	798	1	1.2	652	1	HS7D_WANSE	Q9u639 manduca sex
726	1	1.2	641	1	DNAX_RHIME	P42374 rhizobium m	799	1	1.2	652	1	HS7E_SPIOL	P29357 spinacia ol
727	1	1.2	641	1	HS71_BOVIN	Q27975 bos taurus	800	1	1.2	653	1	HS70_LEIDO	P17804 leishmania
728	1	1.2	641	1	HS71_HUMAN	P08107 homo sapien	801	1	1.2	653	1	HS72_ARATH	P22954 arabidopsis
729	1	1.2	641	1	HS71_MOUSE	P17879 mus musculus	802	1	1.2	654	1	DNAX_CHLMU	P56836 chlamydia m
730	1	1.2	641	1	HS71_PIG	Q07439 sus scrofa	803	1	1.2	654	1	GR78_HUMAN	P11021 homo sapien
731	1	1.2	641	1	HS71_RAT	P10591 saccharomyc	804	1	1.2	654	1	GR78_MESAU	P07823 mesocricetu
732	1	1.2	641	1	HS72_YEAST	Q27965 bos taurus	805	1	1.2	654	1	GR78_RAT	P06761 rattus norv
733	1	1.2	641	1	HS72_BOVIN	P02824 drosophila	806	1	1.2	654	1	HS70_HYDRA	Q05944 hydra magni
734	1	1.2	641	1	HS72_DROME	P55063 rattus norv	807	1	1.2	654	1	HS77_YEAST	P12398 saccharomyc
735	1	1.2	641	1	HS73_RAT	P22202 saccharomyc	808	1	1.2	655	1	YQO9_SCHPO	O13674 schizosacch
736	1	1.2	641	1	HS74_YEAST	P29843 drosophila	809	1	1.2	655	1	GR78_MOUSE	P20029 mus musculu
737	1	1.2	641	1	HS74_DROME	P16627 mus musculu	810	1	1.2	655	1	GR78_PLAFO	Q05866 plasmodium
738	1	1.2	641	1	HS7H_HUMAN	P34931 homo sapien	811	1	1.2	655	1	HS70_DAUCA	P26791 daucus caro
739	1	1.2	641	1	DNAX_FRATU	Q9jvq9 neisseria m	812	1	1.2	655	1	HS71_CANAL	P41797 candida alb
740	1	1.2	642	1	DNAX_NEIMA	Q9k0n4 neisseria m	813	1	1.2	655	1	TR21_MOUSE	Q9epu5 mus musculu
741	1	1.2	642	1	DNAX_NEIMB	P82910 drosophila	814	1	1.2	655	1	YS44_CAEEL	Q09372 caenorhabdi
742	1	1.2	642	1	HS70_DROME	P53623 pichia angu	815	1	1.2	656	1	DNAX_ALCEU	O33522 alcaligenes
743	1	1.2	642	1	HS72_PICAN	P27400 simian foam	816	1	1.2	656	1	DNAX_COXBU	O87712 coxiella bu
744	1	1.2	642	1	GAG_SFV3L	P03918 cladosporiu	817	1	1.2	656	1	HS71_TRYCR	P20583 trypanosoma
745	1	1.2	643	1	HS70_CLAHE	Q10265 schizosacch	818	1	1.2	656	1	HS7C_DROME	P29844 drosophila
746	1	1.2	643	1	HS71_DROME	P02825 drosophila	819	1	1.2	657	1	HS7F_CAEEL	P11141 caenorhabdi
747	1	1.2	643	1	HS71_SCHPO	Q12655 schizosacch	820	1	1.2	658	1	GR78_XENLA	Q91883 xenopus lae
748	1	1.2	643	1	HS76_HUMAN	P17066 homo sapien	821	1	1.2	659	1	DNAX_CHLTR	P17821 chlamydia t
749	1	1.2	643	1	HS76_PIG	Q04967 sus scrofa	822	1	1.2	660	1	DNAX_CHLPN	P27542 chlamydia p
750	1	1.2	643	1	MTR2_HUMAN	Q13614 homo sapien	823	1	1.2	661	1	DHSA_DROME	Q94523 drosophila
751	1	1.2	644	1	DNAX_LEGPN	Q32482 legionella	824	1	1.2	661	1	HS7C_CAEEL	P11145 trypanosoma
752	1	1.2	644	1	DNAX_NITEU	O06430 nitrosomona	825	1	1.2	661	1	GR78_NEUCR	P27420 caenorhabdi
753	1	1.2	644	1	HS70_BRUMA	P27541 brugia mala	826	1	1.2	662	1	SL51_RABIT	P78695 neurospora
754	1	1.2	644	1	HS70_ONCTS	Q91233 oncorhynch	827	1	1.2	662	1	BIP2_MAIZE	P11170 oryctolagus
755	1	1.2	644	1	HS71_PICAN	P53421 pichia angu	828	1	1.2	663	1	BIP3_MAIZE	P24067 ze mays (m
756	1	1.2	644	1	HS71_PICAN	P27322 lycopersico	829	1	1.2	663	1	GR78_SCHPO	Q24581 ze mays (m
757	1	1.2	644	1	VEI_HPV33	P06421 human papil	830	1	1.2	664	1	DEL1_CAEEL	P36804 schizosacch
758	1	1.2	644	1	YED0_YEAST	P26543 human papil	831	1	1.2	664	1	DHSA_HUMAN	Q19038 caenorhabdi
759	1	1.2	644	1	DNAX_LEPIN	P39987 saccharomyc	832	1	1.2	664	1	SL51_SHEEP	P31040 homo sapien
760	1	1.2	645	1	HS70_WAIZE	P71442 leptospira	833	1	1.2	665	1	DHSA_BOVIN	P53791 ovis aries
761	1	1.2	645	1	HS70_WAIZE	Q91291 pleurodeles	834	1	1.2	666	1	BIP_LYCES	P31039 bos taurus
762	1	1.2	645	1	HS70_WAIZE		835	1	1.2	666	1	POL_FMD	P49118 lycopersico
763	1	1.2	645	1	HS70_WAIZE		836	1	1.2	666	1		P09523 figwort mos

837	6	1.2	667	1	BIP4_TORAC	Q03684 nicotiana t	910	6	1.2	763	1	RGT2_YEAST	Q12300 saccharomyc
838	6	1.2	667	1	GR78_APLCA	Q16956 alysia cal	911	6	1.2	769	1	HCRA_THAAR	Q33819 thauera aro
839	6	1.2	668	1	BIP2_ARATH	Q39043 arabidopsis	912	6	1.2	771	1	DNK3_SYNY3	P73098 synechocyst
840	6	1.2	668	1	BIP5_TORAC	Q03685 nicotiana t	913	6	1.2	772	1	YICI_ECOLI	P31434 escherichia
841	6	1.2	668	1	BIP_SPIOI	Q42434 spinacia ol	914	6	1.2	773	1	AD11_MOUSE	Q9rlv4 mus musculus
842	6	1.2	669	1	BIP1_ARATH	Q91kr3 arabidopsis	915	6	1.2	776	1	SM4F_RAT	Q9rlv4 mus musculus
843	6	1.2	669	1	EXL1_MOUSE	Q91kr7 mus musculus	916	6	1.2	776	1	VP4_ROTTP5	P25174 porcine tot
844	6	1.2	670	1	GR78_YARLI	Q99170 yarrowia li	917	6	1.2	776	1	VP4_ROTTP5	P25174 porcine tot
845	6	1.2	670	1	ILVB_ARATH	Q17597 arabidopsis	918	6	1.2	777	1	SM4F_MOUSE	Q92123 mus musculus
846	6	1.2	670	1	YAYE_SCHPO	Q10222 schizosacch	919	6	1.2	777	1	SM4F_MOUSE	Q92123 mus musculus
847	6	1.2	673	1	SM4B_HUMAN	P22774 schizosacch	920	6	1.2	781	1	NANH_VIBCH	Q90763 gallus gall
848	6	1.2	674	1	HS7M_SCHPO	O87906 bacillus th	921	6	1.2	785	1	CAD7_CHICK	P44408 naemophilus
849	6	1.2	675	1	CPAA_BACTJ	P37900 pisum sativ	922	6	1.2	788	1	REC2_HAEIN	P39961 saccharomyc
850	6	1.2	675	1	HS7M_PEA	Q01899 phaseolus v	923	6	1.2	794	1	YE14_YEAST	P39888 saccharomyc
851	6	1.2	676	1	HS7M_PHAVU	P16394 breimia lact	924	6	1.2	796	1	YH04_YEAST	Q9y5e1 homo sapien
852	6	1.2	676	1	HS70_BRELC	O35501 cricetus	925	6	1.2	797	1	CD99_HUMAN	P28968 equine herp
853	6	1.2	679	1	GR75_CRIGR	P38647 mus musculus	926	6	1.2	797	1	VGLX_HSVB	Q96215 thermus aqu
854	6	1.2	679	1	GR75_MOUSE	P48721 rattus norv	927	6	1.2	801	1	CADK_HUMAN	Q92123 mus musculus
855	6	1.2	679	1	GR75_MOUSE	P22010 kluyveromyc	928	6	1.2	811	1	MUTS_THEAQ	Q90763 gallus gall
856	6	1.2	679	1	GR75_MOUSE	P05456 trypanosoma	929	6	1.2	811	1	PMAX_ARATH	P39961 saccharomyc
857	6	1.2	679	1	GR78_KLULA	P11144 plasmodium	930	6	1.2	813	1	YH04_YEAST	P39888 saccharomyc
858	6	1.2	680	1	HS70_TRYCR	P16474 saccharomyc	931	6	1.2	814	1	YH04_YEAST	Q9y5e1 homo sapien
859	6	1.2	681	1	HS70_PLAFA	O8276 solanum tub	932	6	1.2	815	1	CD99_HUMAN	P28968 equine herp
860	6	1.2	682	1	GR78_YEAST	O17972 caenorhabdi	933	6	1.2	816	1	VGLX_HSVB	Q96215 thermus aqu
861	6	1.2	682	1	NPHI_CAEL	O10305 oryza pseu	934	6	1.2	816	1	CADK_HUMAN	Q92123 mus musculus
862	6	1.2	682	1	HE66_NPVOP	Q33113 sesamum ind	935	6	1.2	817	1	MUTS_THEAQ	Q90763 gallus gall
863	6	1.2	682	1	NU5C_SESIN	Q9nr61 homo sapien	936	6	1.2	817	1	PMAX_ARATH	P39961 saccharomyc
864	6	1.2	684	1	HS70_PLAFA	O05746 plasmodium	937	6	1.2	818	1	YH04_YEAST	P39888 saccharomyc
865	6	1.2	685	1	DL14_HUMAN	Q9w6y1 oryza lat	938	6	1.2	819	1	YH04_YEAST	Q9y5e1 homo sapien
866	6	1.2	686	1	HS7C_ORYLA	P29845 drosophila	939	6	1.2	826	1	CD99_HUMAN	P28968 equine herp
867	6	1.2	687	1	HS7E_DROME	Q9zej6 anabaena sp	940	6	1.2	830	1	VGLX_HSVB	Q96215 thermus aqu
868	6	1.2	688	1	DNK1_ANASP	O05714 anabaena va	941	6	1.2	830	1	CADK_HUMAN	Q92123 mus musculus
869	6	1.2	688	1	DNK1_ANASP	P10259 mouse mamma	942	6	1.2	831	1	MUTS_THEAQ	Q90763 gallus gall
870	6	1.2	688	1	ENV_MMTVB	P03374 mouse mamma	943	6	1.2	831	1	PMAX_ARATH	P39961 saccharomyc
871	6	1.2	688	1	ENV_MMTVB	Q91641 xenopus lae	944	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
872	6	1.2	688	1	TH1B_XENLA	O01639 choristoneu	945	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
873	6	1.2	690	1	E75_CHOPU	P16603 saccharomyc	946	6	1.2	833	1	YH04_YEAST	P28968 equine herp
874	6	1.2	690	1	NCPR_YEAST	O58154 synechocyst	947	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu
875	6	1.2	692	1	DNK1_SYNY3	P35655 pseudomonas	948	6	1.2	833	1	YH04_YEAST	Q92123 mus musculus
876	6	1.2	695	1	HRPI_PSEY	Q9vc27 drosophila	949	6	1.2	833	1	YH04_YEAST	Q90763 gallus gall
877	6	1.2	695	1	NICA_DROME	Q08893 manduca sex	950	6	1.2	833	1	YH04_YEAST	P39961 saccharomyc
878	6	1.2	699	1	E75_MANSE	Q9ukm7 homo sapien	951	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
879	6	1.2	699	1	M1B1_HUMAN	P23327 rattus norv	952	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
880	6	1.2	699	1	SRCH_HUMAN	P16235 rattus norv	953	6	1.2	833	1	YH04_YEAST	P28968 equine herp
881	6	1.2	700	1	LSHR_RAT	P09552 micrococ	954	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu
882	6	1.2	701	1	EFG_MICLU	O75342 homo sapien	955	6	1.2	833	1	YH04_YEAST	Q92123 mus musculus
883	6	1.2	701	1	LOXR_HUMAN	O70582 mus musculus	956	6	1.2	833	1	YH04_YEAST	Q90763 gallus gall
884	6	1.2	701	1	LOXR_MOUSE	O00043 ajellomyces	957	6	1.2	833	1	YH04_YEAST	P39961 saccharomyc
885	6	1.2	701	1	HS70_AJECA	Q02028 pisum sativ	958	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
886	6	1.2	705	1	HS75_PEA	Q9mv16 malvaviscus	959	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
887	6	1.2	706	1	NU5C_MALAR	P05335 candida mal	960	6	1.2	833	1	YH04_YEAST	P28968 equine herp
888	6	1.2	707	1	CA04_CANMA	P57716 mus musculus	961	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu
889	6	1.2	708	1	NICA_MOUSE	O29542 homo sapien	962	6	1.2	833	1	YH04_YEAST	Q92123 mus musculus
890	6	1.2	708	1	NICA_MOUSE	Q9mwk2 pachira aqu	963	6	1.2	833	1	YH04_YEAST	Q90763 gallus gall
891	6	1.2	709	1	NICA_HUMAN	P11420 drosophila	964	6	1.2	833	1	YH04_YEAST	P39961 saccharomyc
892	6	1.2	709	1	NU5C_PACAO	P50239 gallieria me	965	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
893	6	1.2	710	1	DA_DROME	O03274 popillia ja	966	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
894	6	1.2	711	1	E75_GALME	P31835 paenibacill	967	6	1.2	833	1	YH04_YEAST	P28968 equine herp
895	6	1.2	711	1	PO22_POPJA	P04830 paenibacill	968	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu
896	6	1.2	713	1	CDG2_PAEPA	P58722 yersinia pe	969	6	1.2	833	1	YH04_YEAST	Q92123 mus musculus
897	6	1.2	714	1	CDG1_PAEPA	O00423 homo sapien	970	6	1.2	833	1	YH04_YEAST	Q90763 gallus gall
898	6	1.2	715	1	IGAA_YERPE	Q9m7j4 nicotiana t	971	6	1.2	833	1	YH04_YEAST	P39961 saccharomyc
899	6	1.2	717	1	EMLI_HUMAN	O96rq3 homo sapien	972	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
900	6	1.2	722	1	MFPI_TOBAC	P15502 homo sapien	973	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
901	6	1.2	725	1	MCCA_HUMAN	Q46631 erwinia amy	974	6	1.2	833	1	YH04_YEAST	P28968 equine herp
902	6	1.2	726	1	AMSA_ERWAM	P15502 homo sapien	975	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu
903	6	1.2	730	1	ELS_HUMAN	P33145 gallus gall	976	6	1.2	833	1	YH04_YEAST	Q92123 mus musculus
904	6	1.2	732	1	CADL_CHICK	O9gz66 homo sapien	977	6	1.2	833	1	YH04_YEAST	Q90763 gallus gall
905	6	1.2	736	1	NTT5_HUMAN	Q9x6b0 yersinia pe	978	6	1.2	833	1	YH04_YEAST	P39961 saccharomyc
906	6	1.2	737	1	CATA_YERPE	P50022 synechococ	979	6	1.2	833	1	YH04_YEAST	P39888 saccharomyc
907	6	1.2	749	1	DNK3_SYNP7	O9tlc2 tecoma stan	980	6	1.2	833	1	YH04_YEAST	Q9y5e1 homo sapien
908	6	1.2	750	1	NU5C_TECST	Q9rlw9 corynebacte	981	6	1.2	833	1	YH04_YEAST	P28968 equine herp
909	6	1.2	758	1	PURL_CORAM		982	6	1.2	833	1	YH04_YEAST	Q96215 thermus aqu

983 6 1.2 975 1 CLTM_YEAST
 984 6 1.2 991 1 GBRL_RAT
 985 6 1.2 994 1 SVL_XYLFA
 986 6 1.2 1007 1 CHC2_HUMAN
 987 6 1.2 1014 1 EPB6_MOUSE
 988 6 1.2 1015 1 FONG_ECOLI
 989 6 1.2 1015 1 YRD3_CAEEL
 990 6 1.2 1020 1 ITA4_DROME
 991 6 1.2 1025 1 PO21_NSVI
 992 6 1.2 1026 1 DHE2_NEUCR
 993 6 1.2 1030 1 STK9_HUMAN
 994 6 1.2 1030 1 VPPL_CAEEL
 995 6 1.2 1038 1 BMR2_HUMAN
 996 6 1.2 1038 1 BMR2_MOUSE
 997 6 1.2 1042 1 ATHL_BUFMA
 998 6 1.2 1043 1 DSG1_BOVIN
 999 6 1.2 1044 1 ITA8_CHICK
 1000 6 1.2 1046 1 K052_HUMAN

ALIGNMENTS

RESULT 1
 ID ARSB_STAAU STANDARD; PRT; 429 AA.
 AC P30329;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Arsenical pump membrane protein.
 DE ARSB.
 OS Staphylococcus aureus.
 GN Plasmid p1258.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CC NCBI_TaxID=1280;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=92276351; PubMed=1534328;
 CC JI G., Silver S.;
 CC "Regulation and expression of the arsenic resistance operon from
 CC Staphylococcus aureus plasmid p1258.";
 CC J. Bacteriol. 174:3684-3694(1992).
 CC -!- FUNCTION: INVOLVED IN ARSENICAL RESISTANCE. THOUGHT TO FORM THE
 CC CHANNEL OF AN ARSENITE PUMP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC
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 CC
 CC EMBL; M06824; AAA25637.1; -
 CC PIR; C41903;
 CC InterPro; IPR000802; Ars_pump.
 CC Pfam; PF02040; Arsb; 1.
 CC PRINTS; PR00758; ARSENICPUMP.
 CC TIGRFAMS; TIGR00935; 2a45; 1.
 CC Plasmid; Arsenical resistance; Transmembrane.
 CC SEQUENCE 429 AA; 46484 MW; 654CE9BA110A15DB CRC64;

Query Match 1.6%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 IVLAVLLV 437
 DB 230 IVLAVLLV 237

RESULT 2
 ID VES_HPV33 STANDARD; PRT; 75 AA.
 AC P06426;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Probable E5 protein.
 DE VES.
 GN Human papillomavirus type 33.
 OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Papillomavirus.
 CC NCBI_TaxID=10586;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=86200464; PubMed=3009902;
 CC Cole S.T., Streeck R.E.;
 CC "Genome organization and nucleotide sequence of human papillomavirus
 CC type 33, which is associated with cervical cancer.";
 CC J. Virol. 58:991-995(1986).
 CC
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 CC
 CC EMBL; M12732; AAA46962.1; -
 CC PIR; A03679; W5WL33.
 CC InterPro; IPR004270; Papilloma_E5.
 CC Pfam; PF03025; Papilloma_E5; 1.
 CC Early protein.
 CC SEQUENCE 75 AA; 8906 MW; CDC414CA37052CA8 CRC64;
 CC
 CC Query Match 1.4%; Score 7; DB 1; Length 75;
 CC Best Local Similarity 100.0%; Pred. No. 11;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLLVLVL 12
 DB 31 WLLVLVL 37

RESULT 3
 ID VES_HPV58 STANDARD; PRT; 76 AA.
 AC R26552;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Probable E5 protein.
 DE VES.
 GN Human papillomavirus type 58.
 OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Papillomavirus.
 CC NCBI_TaxID=10598;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=92024102; PubMed=1656594;
 CC Kirii Y., Iwamoto S., Matsukura T.;
 CC "Human papillomavirus type 58 DNA sequence.";
 CC Virology 185:424-427(1991).
 CC
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DR EMBL; D90400; BAA31849.1;
DR PIR; D36779; W5WLS8;
DR InterPro; IPR004270; Papilloma_E5;
DR Pfam; PF03025; Papilloma_E5; 1;
KW Early protein.
SQ SEQUENCE 76 AA; 8953 MW; C4B6E29BC1D6BA76 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLIVLVL 12
DB 32 WLIVLVL 38

RESULT 4
VG9_SpVIR STANDARD; PRT; 78 AA.
AC P15900;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Gene 9 protein.
GN 9.
OS Spiroplasma virus SpV1-R8A2 B.
OC Viruses; ssDNA viruses; Inoviridae; Plectrovirus.
OX NCBI_TaxID=10854;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90206799; PubMed=2320423;
RA Renaudin J., Aulio P., Vignault J.C., Bove J.M.;
RT "Complete nucleotide sequence of the genome of Spiroplasma citri
virus SpV1-R8A2 B.";
RL Nucleic Acids Res. 18:1293-1293(1990).

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QY 434 VLLVAAL 440
DB 12 VLLVAAL 18

RESULT 6
GALP_PIG STANDARD; PRT; 120 AA.
ID GALP_PIG
AC Q9RT95;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Galanin-like peptide precursor.
GN GALP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A... SEQUENCE OF 23-82, AND SYNTHESIS OF 23-82.
RX TISSUE=Hypothalamus;
RX MEDLINE=20069685; PubMed=10601261;
RA Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,
RA Kitada C., Kurokawa T., Onda H., Fujino M.;
RT "Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
from porcine hypothalamus.";
RL J. Biol. Chem. 274:37041-37045(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.

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EMBL; AF188490; AAF19722.1;
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 22
FT PEPTIDE 23 82
FT PROPEP 85 120

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SQ SEQUENCE 120 AA; 12681 MW; 709F7DBF42149054 CRC64;
Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 IVLAVILL 436
|||||
DB 8 IVLAVILL 14

RESULT 7
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P05136;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain 6/82) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11121;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86286562; PubMed=3016650;
RA Binns M.M., Boursnell M.E.G., Tomley F.M., Brown T.D.K.;
RT "Nucleotide sequence encoding the membrane protein of the IBV strain 6/82.";
RL Nucleic Acids Res. 14:5558-5558(1986).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X04107; CAA27727.1; -
DR EMBL; D00005; BAA00003.1; -
DR PIR; A23649; MWIH68.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25465 MW; AF4612BFBFC2EF7 CRC64;

Query Match
Best Local Similarity 1.4%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

RESULT 8
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P04327;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain Beaudette M42) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11123;
RN [1]
RP SEQUENCE.
RX MEDLINE=88007845; PubMed=2821010;
RA Machamer C.E., Rose J.K.;
RT "A specific transmembrane domain of a coronavirus E1 glycoprotein is required for its retention in the Golgi region.";
RL J. Cell Biol. 105:1205-1214(1987).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
DR EMBL; M95169; AAA70239.1; -
DR EMBL; M22014; AAA46215.1; -
DR PIR; A04022; MWIHIV.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25475 MW; D5AE8685CF78220D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

RESULT 9
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P11222;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain Beaudette M42) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11123;
RN [1]
RP SEQUENCE.
RX MEDLINE=88007845; PubMed=2821010;
RA Machamer C.E., Rose J.K.;
RT "A specific transmembrane domain of a coronavirus E1 glycoprotein is required for its retention in the Golgi region.";
RL J. Cell Biol. 105:1205-1214(1987).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
DR EMBL; M95169; AAA70239.1; -
DR EMBL; M22014; AAA46215.1; -
DR PIR; A04022; MWIHIV.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25475 MW; D5AE8685CF78220D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

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DR Pfam: PF01635; Corona_M; 1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).
FT TRANSMEM 21 42 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 78 101 POTENTIAL.
SQ SEQUENCE 225 AA; 25477 MW; 466349883C7B2D21 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 436 LVAAIIL 442
Db 79 LVAAIIL 85

RESULT 10
VMEI_IBVK
ID VMEI_IBVK STANDARD; PRT; 225 AA.
AC P12649;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain KB8523) (IBV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11126;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89306251; PubMed=2841803;
RA Sutou S., Sato S., Okabe T., Nakai M., Sasaki N.;
RT "Cloning and sequencing of genes encoding structural proteins of
RT avian infectious bronchitis virus.";
RL Virology 165:589-595(1988).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE
CC IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
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CC -----
CC EMBL; M21515; AAA6581.1; -
DR PIR; C29249; MMIHAI.
DR InterPro; IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25541 MW; F76DA96A71416932 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 436 LVAAIIL 442
Db 79 LVAAIIL 85

RESULT 11

VGI6_BPPHC
ID VGI6_BPPHC STANDARD; PRT; 237 AA.
AC Q9ZX92;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gene 16 protein (GP16).
GN 16.
OS Bacteriophage phi-C31.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Norwich stock;
RX MEDLINE=99162580; PubMed=10051617;
RA Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;
RT "Evolutionary relationships among diverse bacteriophages and
RT prophages: all the world's a phage."
RL Proc. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999).
CC -!- SIMILARITY: BELONGS TO THE THY1 FAMILY.
CC -----
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CC -----
CC EMBL; AJ006589; CAA07140.1; -
DR InterPro; IPR003669; Thyl.
DR Pfam: PF02511; Thyl; 1.
SQ SEQUENCE 237 AA; 26016 MW; 3FDEF9BA6DF302C0 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 REAARAL 19
Db 165 REAARAL 171

RESULT 12
YCXE_BACME
ID YCXE_BACME STANDARD; PRT; 286 AA.
AC P40419;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.5 kDa protein in gdh1 5' region (ORF 2).
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM 1030;
RA Mitamura T., Ebara R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
RA Okada H.;
RT "Structure of isozyme genes of glucose dehydrogenase from Bacillus
RT megaterium IAM1030."
RL J. Ferment. Bioeng. 70:363-369(1990).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPOULATION.
CC -!- SIMILARITY: TO A SIMILAR ORF IN B.SUBTILIS.
CC -----
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CC -----
DR EMBL; D90043; BAA14098.1; -
DR PIR; JS0384;
DR InterPro; IPR000620; DUF6.
DR InterPro; IPR004673; RhaT.
DR Pfam; PF00892; DUF6; 1.
DR TIGRfams; TIGR00776; RhaT; 1.
KW Hypothetical protein; Sporulation.
SQ SEQUENCE 286 AA; 30490 MW; 95AB89D02511D74D CRC64;

Query Match 1.4%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 IVGIVLA 433
DB 127 IVGIVLA 133
|||||

RESULT 13
V084_HSV6U
ID V084_HSV6U STANDARD; PRT; 342 AA.
AC P52532;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein U84.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
GN Herpesviridae; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95027704; PubMed=7941342;
RA Nicholas J.;
RT "Nucleotide sequence analysis of a 21-kbp region of the genome of
RT human herpesvirus-6 containing homologues of human cytomegalovirus
RT major immediate-early and replication genes.";
RL Virology 204:738-750(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution.";
RL Virology 209:29-51(1995).
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U84 AND HCMV UL117.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U13194; AAA68475.1; -
DR EMBL; X83413; CAA58333.1; -
SQ SEQUENCE 342 AA; 39555 MW; 2AF4C6BDEC729C74 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 LQNNLSP 415
DB 46 LQNNLSP 52
|||||

RESULT 14

```

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INVE_SALTY
ID INVE_SALTY STANDARD; PRT; 372 AA.
AC P35671;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Invasion protein invE.
GN INVE OR STM2897.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR11 / SL1344;
RX MEDLINE=92335220; PubMed=1631083;
RA Ginocchio C., Pace J., Galan J.E.;
RT "Identification and molecular characterization of a Salmonella
RT typhimurium gene involved in triggering the internalization of
RT salmonellae into cultured epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5976-5980(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RN [3]
RP Nature 413:852-856(2001).
RX SEQUENCE OF 1-69 FROM N.A.
RP STRAIN=SR-11;
RX MEDLINE=95089692; PubMed=7997169;
RA Kaniga K., Bossio J.C., Galan J.E.;
RT "The Salmonella typhimurium invasion genes invF and invG encode
RT homologues of the AraC and Pvd family of proteins.";
RL Mol. Microbiol. 13:555-568(1994).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RX STRAIN=TM1;
RX MEDLINE=95172719; PubMed=7868245;
RA Lodge J., Douce G.R., Amin I.I., Bolton A.J., Martin G.D.,
RA Chatfield S., Dougan G., Brown N.L., Stephen J.;
RT "Biological and genetic characterization of TnphoA mutants of
RT Salmonella typhimurium TML in the context of gastroenteritis.";
RL Infect. Immun. 63:762-769(1995).
CC -!- FUNCTION: INVOLVED IN THE TRIGGERING OF INTRACELLULAR EVENTS THAT
CC LEAD TO MICROBIAL INTERNALIZATION OF THE INTESTINAL EPITHELIUM.
CC THESE EVENTS INCLUDE INCREASE IN CALCIUM LEVEL, REDISTRIBUTION OF
CC ACTIN MICROFILAMENTS, AND CHANGES IN THE NORMAL STRUCTURE OF THE
CC MICROVILLI.
CC -!- SIMILARITY: TO YERSINIA OUTER MEMBRANE PROTEIN YOPN (LCRE).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M90714; -; NOT_ANNOTATED_CDS.
DR EMBL; AE008832; AAG21777.1; -
DR EMBL; U08280; AAA74041.1; -
DR EMBL; X75302; CAA53050.2; -
DR StyGene; SG10187; invE.
DR InterPro; IPR003520; Invas_invE.
DR Pfam; PF02523; invE; 1.
KW Virulence; Complete proteome.

```

FT CONFLICT 64 64 Q -> E (IN REF. 1 AND 3).
 FT CONFLICT 117 117 S -> T (IN REF. 1).
 SQ SEQUENCE 372 AA; 42421 MW; 7E10B570D2AF644F CRC64;

Query Match 1.4%; Score 7; DB 1; Length 372;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LVLVIRE 14
 DB 125 LVLVIRE 131

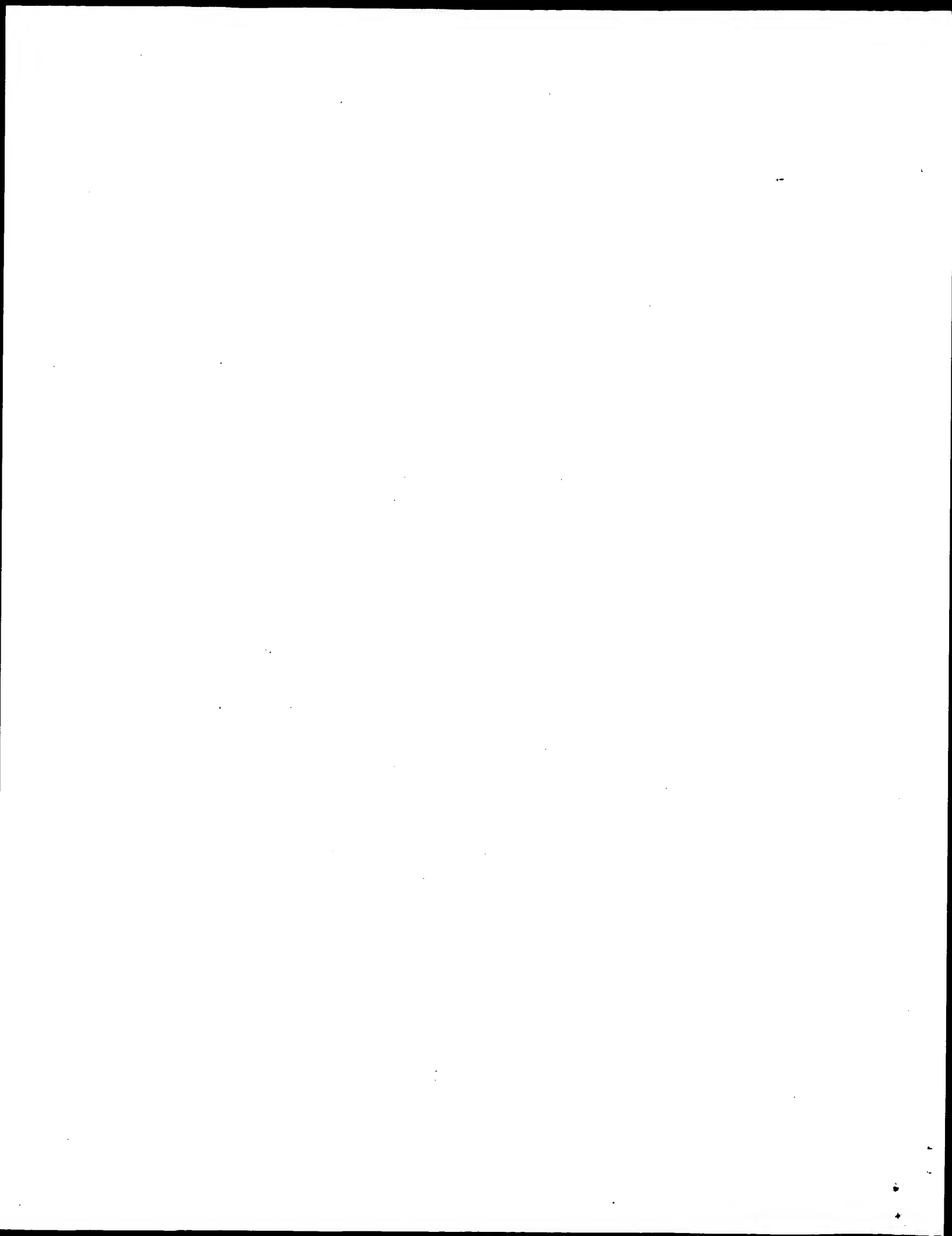
RESULT 15

FTSW_HELPJ STANDARD; PRT; 388 AA.
 AC Q92J48;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable cell division protein ftsw.
 GN FTSW OR JHP1468.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -!- FUNCTION: THIS IS A SEPTUM-PEPTIDOGLYCAN BIOSYNTHETIC PROTEIN,
 CC INVOLVED IN CELL WALL FORMATION. PLAYS A ROLE IN THE STABILIZATION
 CC OF THE FTSZ RING DURING CELL DIVISION (BY SIMILARITY). Inner membrane
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE001568; AAD07042.1; -;
 CC InterPro; IPR001182; Cell-cycle.
 CC Pfam; PF01098; FTSW_RODA_SPOVE; 1.
 CC PROSITE; PS00428; FTSW_RODA_SPOVE; 1.
 CC Peptidoglycan synthesis; Cell wall; Cell division; Cell shape;
 CC Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 7 27 POTENTIAL.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 FT TRANSMEM 145 165 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 262 282 POTENTIAL.
 FT TRANSMEM 295 315 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 359 379 POTENTIAL.
 SQ SEQUENCE 388 AA; 42540 MW; 51E4277A910B286D CRC64;

Query Match 1.4%; Score 7; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 VLAVLLV 437
 DB 178 VLAVLLV 184

Search completed: April 22, 2003, 16:17:04
 Job time : 32 secs



GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:03:25 ; Search time 34 Seconds
(without alignments)
3030.105 Million cell updates/sec

Title: 'US-09-918-715-230
Perfect score: 2691
Sequence: 1 MRCELWLLVLRARALS.....YAEVPSGHEKSGFMEDQC 500

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2691	100.0	500	4	Q9HCT9		Q9hct9 homo sapien
2	2209	82.1	500	11	Q91ZV7		Q91zv7 mus musculu
3	2203	81.9	500	11	Q9CWV5		Q9cww5 mus musculu
4	1295	48.1	529	4	Q96PD9		Q96pd9 homo sapien
5	1275.5	47.4	530	11	Q9DC11		Q9dcl1 mus musculu
6	1275.5	47.4	530	11	Q91ZV6		Q91zv6 mus musculu
7	1127.5	41.9	480	4	Q96E59		Q96e59 homo sapien
8	660.5	24.5	625	5	Q9WZV9		Q9wzv9 drosophila
9	611	22.7	476	5	Q18500		Q18500 caenorhabdi
10	297.5	11.1	151	4	Q96S09		Q96su9 homo sapien
11	126	4.7	1161	5	Q04901		Q04901 halocynthia
12	117	4.3	308	4	Q9UN94		Q9un94 homo sapien
13	115.5	4.3	1568	4	Q60486		Q60486 homo sapien
14	111.5	4.1	366	4	Q9UN95		Q9un95 homo sapien
15	111.5	4.1	877	4	Q9H306		Q9h3q6 homo sapien
16	111.5	4.1	878	4	Q9H307		Q9h3q7 homo sapien

Q9ukw9 homo sapien
Q9hl95 homo sapien
Q9gzz2 homo sapien
Q9flf3 streptococ
Q9fb48 corynebacte
Q9fvr3 arabidopsis
Q9r4u3 mus musculu
Q9ly36 mus musculu
Q68868 synechococc
Q54916 mus musculu
Q9fls3 streptococ
Q9vly7 ephydatia f
Q9lma7 arabidopsis
Q96d71 homo sapien
Q9bxy9 homo sapien
Q9gta4 leishmania
Q9r4u4 rattus norv
Q9av18 oryza sativ
Q8tbd9 homo sapien
Q9ug37 homo sapien
Q9hca1 homo sapien
Q9v4b6 homo sapien
Q13446 caenorhabdi
Q9sxx8 nicotiana t
P90662 aedes aegypt
Q9flj8 arabidopsis
Q9qzc2 mus musculu
Q08758 mus musculu
Q57106 inkoo virus

ALIGNMENTS

RESULT 1

Q9HCT9 PRELIMINARY; PRT; 500 AA.
ID Q9HCT9;
AC Q9HCT9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor (Tumor endothelial marker 3 precursor).
DE TM7.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RA "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA St Croix B., Vogelstein B., Kinzler K.W.;
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carlson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RN "Cell surface tumor endothelial markers are conserved in mice and humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF279144; AAC00869.2; -;
DR EMBL; AF378753; AAL11990.1; -;
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR002165; Flexin_repeat.
DR InterPro; IPR003975; Shal_channel.

```

DR Pfam: PF01437; PSI: 1.
DR Signal: 1 18 POTENTIAL.
DR SMART: SM00539; NIDO; 1.
FT CHAIN 19 500 TUMOR ENDOTHELIAL MARKER 3.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 500 TUMOR ENDOTHELIAL MARKER 7.
SO SEQUENCE 500 AA: 55760 MW; C545A16619EEDEBED CRC64;

Query Match 100.0%; Score 2691; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.5e-232;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLLVREARALSPQAGHDEGPGSGWAAKGTGVGNRRRARESPGHVSEPD 60
DB 1 MRGELWLLVLLVREARALSPQAGHDEGPGSGWAAKGTGVGNRRRARESPGHVSEPD 60
QY 61 TOLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 120
DB 61 TOLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 120
QY 121 IHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSSOHPVKTGILSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFT 300
DB 241 SVPEISSSOHPVKTGILSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFT 300
QY 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFQ 360
QY 361 DEHDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKGT 420
DB 361 DEHDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVEPSGHEKEGFEAEQC 500
DB 481 YAEVEPSGHEKEGFEAEQC 500

RESULT 2
Q912V7 ID Q912V7 PRELIMINARY; PRT; 500 AA.
AC Q912V7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Tumor endothelial marker 7 precursor.
GN 2410003107RIK OR TEW7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans."
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378760; AAL11997.1; -
DR MGI; MGI:1919574; 2410003107RIK.
DR InterPro; IPR002165; Plexin_repeat.

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DR Pfam: PF01437; PSI: 1.
DR Signal: 1 19 POTENTIAL.
DR SMART: SM00539; NIDO; 1.
FT CHAIN 20 500 TUMOR ENDOTHELIAL MARKER 7.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 500 TUMOR ENDOTHELIAL MARKER 7.
SO SEQUENCE 500 AA: 55693 MW; 14FE25512A319DAF CRC64;

Query Match 82.1%; Score 2209; DB 11; Length 500;
Best Local Similarity 81.6%; Pred. No. 6e-189;
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

QY 1 MRGELWLLVLLVREARALSPQAGHDEGPGSGWAAKGTGVGNRRRARESPGHVSEPD 59
DB 1 MRGELWLLVLLVREARALSPQAGHDEGPGSGWAAKGTGVGNRRRARESPGHVSEPD 59
QY 60 RTOLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 119
DB 60 RTOLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 119
QY 61 KTQLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 120
DB 61 KTQLSDQLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAENRSQV 120
QY 120 KIHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 179
DB 120 KIHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 179
QY 121 KIHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 KIHTILSNTHRQASRVVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 180 ANENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIP 239
DB 180 ANENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIP 239
QY 181 ANENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIP 240
DB 181 ANENPGYSNSTVYVDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIP 240
QY 240 MSVPEISSSOHPVKTGILSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFT 299
DB 240 MSVPEISSSOHPVKTGILSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFT 299
QY 241 MAYLDISSAOPHVKAGLSDAFMIINSSPEVPSQRRTIFEYHRIELDPKVTSMGSAVEFT 300
DB 241 MAYLDISSAOPHVKAGLSDAFMIINSSPEVPSQRRTIFEYHRIELDPKVTSMGSAVEFT 300
QY 300 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDF 359
DB 300 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDF 359
QY 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDF 360
DB 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDF 360
QY 360 QDEHDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKG 419
DB 360 QDEHDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKG 419
QY 361 QDSDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKG 419
DB 361 QDSDHSAASPDTSFSDYDGLTTSLSLFDITTTEDDTKLPYAGGDLQNNLSPKTKG 419
QY 420 TPVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 479
DB 420 TPVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 479
QY 480 YAEVEPSGHEKEGFEAEQC 500
DB 480 YAEVEPSGHEKEGFEAEQC 500

RESULT 3
Q9CWV5 ID Q9CWV5 PRELIMINARY; PRT; 500 AA.
AC Q9CWV5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Tumor endothelial marker 7 precursor.
GN 2410003107RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR ENBL: AK010361; BAB26881.1; -;
DR MGD: MGI:1919574; 2410003107Rik.
DR InterPro: IPR003886; Nidogen_ext.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; plexin-repeat.
DR Pfam: PF01437; PSI: 1.
DR SMART: SM00539; NIDO: 1.
DR SMART: SM00423; PSI: 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
Query Match 81.9%; Score 2203; DB 11; Length 500;
Best Local Similarity 81.4%; Pred. No. 2.1e-188;
Matches 408; Conservative 46; Mismatches 45; Indels 2; Gaps 2;
QY 1 MRGELWLL-VLVREAAARALSPQAGHDEGPGSGMAAKGTVRGWNRRARESPGHVSEPD 59
DB 1 MRAQLLQQLLLRGAARALSPATPAGHNEQGSAAWAKTRQGRSRPRSPAQVLKPG 60
QY 60 RTQLSODLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWLDVAEANKRSQV 119
DB 61 KTQLSODLGGSLAIDTLPDNRTRVEDNHNYSYRVYGPCKSQSLWDLAVANRSHV 120
QY 120 KIHRTLSNTHRQASRVLSDFPFYVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIP 179
DB 121 KIHRTLSNTHRQASRVLSDFPFYVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIP 180
QY 180 ANFNPGYSDNSTVYFDNGTVVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIP 239
DB 181 ANFNPGYSDNSTVYFDNGTVVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIP 240
QY 240 MSVPRISSQHPVKTKGLSDFAMILNPSDPVPESSRRSIFEFYHRIELDPKSVTMSAVEFT 299
DB 241 MAVLDISSAHPVKAGLSDFAMILNPSDPVPESSRRSIFEFYHRIELDPKSVTMSAVEFT 300
QY 300 PLPTCLOHSCDACHSSDLTFNCSCWCHVLRCSGDFRYRQWMDYCAQAEAGRMCDPF 359
DB 301 PLPTCLOHSCDACHSSDLTFNCSCWCHVLRCSGDFRYRQWMDYCAQAEAGRMCDPF 360
QY 360 QDEHDSASPDTSFSPYDGLTSTSSFLDSTLTTEDDTKLNYPAGSGDGLQNNLSPKTKG 419
DB 361 QDHSYASPDTSFSPFNGD-STTSSFLDSTLTTEDDTKLNYPAGSGDGLQNNLSPKTKG 419
QY 420 TPVHLGTIVGIVLVAALLVAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHDPHSH 479
DB 420 TPVHLGTIVGIVLVAALLVAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHDPHSH 479
QY 480 TYAEVPSGHEKEGFEAEQC 500
DB 480 TYAEVPSGHEKEGFEAEQC 500
RESULT 4
Q96PD9 PRELIMINARY; PRT; 529 AA.
AC Q96PD9; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
GN TEM7R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.,
RT "Cell surface tumor endothelial markers are conserved in mice and humans";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL: AF378757; AAL11994.1; -;
DR InterPro: IPR002165; Plexin-repeat.
DR Pfam: PF01437; PSI: 1.
KW SIGNAL.
FT SIGNAL. 1 30 POTENTIAL.
FT CHAIN 31 529 TUMOR ENDOTHELIAL MARKER 7-RELATED.
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;
Query Match 48.1%; Score 1295; DB 4; Length 529;
Best Local Similarity 57.3%; Pred. No. 3.9e-107;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;
QY 72 LAMDTLPDNRTRVED-NHSYVSRLYGPSEPHSRELWLDVAEANKRSQVKIHTLSNTHR 130
DB 95 LLLDDGQDNTQTEEDTDHNYISRIYGPDSASDLWVNDIDMEKDKVYHIGILSNTHR 154
QY 131 QASRVLSDFPFYVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSOH 190
DB 155 QAARVNLSDFPFYVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSOH 214
QY 191 TVYVFDNGTVVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSOH 250
DB 215 TVYVFDNGTVVQWHDVHVLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSOH 274
QY 251 PVKTVGLSDFAMILNPSDPVPESSRRSIFEFYHRIELDPKSVTMSAVEFTPLPTCLOHSC 310
DB 275 PVKTVGLSDFAMILNPSDPVPESSRRSIFEFYHRIELDPKSVTMSAVEFTPLPTCLOHSC 334
QY 311 DACWSSDLTFNCSCWCHVLRCSGDFRYRQWMDYCAQAEAGRMCDPFQDEHDSASPD 370
DB 335 GPCVSSQIGFNCSCWCHVLRCSGDFRYRQWMDYCAQAEAGRMCDPFQDEHDSASPD 394
QY 371 T-SFSPYDGLTSTSSFLDSTLTTEDDTKLNYPAGSGDGLQNNLSPKTKGTPVHL 424
DB 395 TIGATTTFQFVLTTRAVTSQFPTSLPTEDDTKIALHLKDNAGSTDDSAEAKKGTLLHA 454
QY 425 GTIVGIVLVAALLVAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHDPHSHYAEV 484
DB 455 GLVIGLILVIVATALTIVTYVYHPTSAASIFFIERRPSPRPAMKFRSGHGPAYAEV 514
QY 485 EPSGHEKEGFEAEQC 500
DB 515 EPVG-EKEGFTVSEQ 529
RESULT 5
Q9DC11 PRELIMINARY; PRT; 530 AA.
AC Q9DC11; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 1200007L24Rik protein.
GN 1200007L24Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casanova T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide J., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momaberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Yushan-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.;
 RL Nature 409:685-690(2001).
 DR EMBL: AK004640; BAB23431.1; -;
 DR MGD: MGI:1914698; 1200007L24Rik.
 DR InterPro: IPR003886; Nidogen_ext.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002165; plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 DR SMART: SM00539; NIDO: 1.
 DR SMART: SM00423; PSI: 1.
 SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 47.4%; Score 1275.5; DB 11; Length 530;
 Best Local Similarity 52.9%; Pred. No. 2.2e-105;
 Matches 248; Conservative 77; Mismatches 129; Indels 15; Gaps 7;

QY 44 WNRARESPGHVSEPDRTQLSQ-----DLGGGTLMADTLPDNRTRVED-NHSYVVSRLYG 98
 Db 65 WKNRV--DPFKAVDNTNRASMGQSPESKGTDLDDGQDNNTQIEDTHNYISRIYG 122
 QY 99 PSEPHSRELWVDVAEANRSOVKIHILSNTHROASRVLSDFDPYGHPLQIATGGF 158
 Db 123 PADSASRLWVNDOMEKDKVKGILSNTHROARVNLSDFFPYGHFLNEVTVATGGF 182
 QY 159 IFMGDVTHRLMTATQYVAPLMAFNPGYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGS 218
 Db 183 IYTGVEVHRLMTATQYIAPLMAFNPDPSVSRNSTVRYFDNGTALVQWHDVHLQDNYNLGS 242
 QY 219 FTFOAALHHDGRIVFAVEKIPMSVPEISSOHVPKVTGLSDAFMLNPSDPVPSRRSIF 278
 Db 243 FTFOATLLMDGRILFYKEIPVLTQISSTNHPVKVGLSDAFVYVHRTTQQIPNVRRTIY 302
 QY 279 EYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDY 338
 Db 303 EYHVELQMSKITNISAVEMTPTCLQFNGCGPCVSSQIGFNCWSKLRQCSGFDH 362
 QY 339 ROEMWYDCAQAEAG--RMCEDFQDEHDSASPDTSFSPYDGLTTS----SSLFIDSL 392
 Db 363 RQWVDSCGPEEVQSKMKCEKTEPGTTSQTTSHTTMOFRVLTTRRAVTSQMPSTL 422
 QY 393 TTEDDTKLNYPAGGDLQ--NLSPKTKGTPVHLGTVIGVLAIVLVAAILAGIYINGHP 451
 Db 423 PTEDDTKIALHLKDSGASTDSDSAEKKGGTLAGLIVLILVLIITAAAILVTVMYVHHP 482
 QY 452 TSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMARQC 500
 Db 483 TSAASIFFIERRPSPKAMKFRSGHPAYAEVPGV-EKEGFIVSEQ 530

RESULT 6

Q912V6 ID Q912V6 PRELIMINARY; PRT; 530 AA.
 AC Q912V6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Tumor endothelial marker 7-related precursor.
 GN 1200007L24RIK OR TEM7R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21443268; PubMed-11559528;
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
 RA Kinzler K.W., St Croix B.;
 RT "Cell surface tumor endothelial markers are conserved in mice and humans."
 RL Cancer Res. 61:6649-6655(2001).
 DR EMBL: AF378761; AALL1198.1; -;
 DR MGD: MGI:1914698; 1200007L24Rik.
 DR InterPro: IPR002165; Plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 KW SIGNAL.
 FT CHAIN 1 30 POTENTIAL.
 FT CHAIN 31 530 TUMOR ENDOTHELIAL MARKER 7-RELATED.
 SQ SEQUENCE 530 AA; 59625 MW; FF8315020735E36D CRC64;

Query Match 47.4%; Score 1275.5; DB 11; Length 530;
 Best Local Similarity 52.9%; Pred. No. 2.2e-105;
 Matches 248; Conservative 77; Mismatches 129; Indels 15; Gaps 7;

QY 44 WNRARESPGHVSEPDRTQLSQ-----DLGGGTLMADTLPDNRTRVED-NHSYVVSRLYG 98
 Db 65 WKNRV--DPFKAVDNTNRASMGQSPESKGTDLDDGQDNNTQIEDTHNYISRIYG 122
 QY 99 PSEPHSRELWVDVAEANRSOVKIHILSNTHROASRVLSDFDPYGHPLQIATGGF 158
 Db 123 PADSASRLWVNDOMEKDKVKGILSNTHROARVNLSDFFPYGHFLNEVTVATGGF 182
 QY 159 IFMGDVTHRLMTATQYVAPLMAFNPGYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGS 218
 Db 183 IYTGVEVHRLMTATQYIAPLMAFNPDPSVSRNSTVRYFDNGTALVQWHDVHLQDNYNLGS 242
 QY 219 FTFOAALHHDGRIVFAVEKIPMSVPEISSOHVPKVTGLSDAFMLNPSDPVPSRRSIF 278
 Db 243 FTFOATLLMDGRILFYKEIPVLTQISSTNHPVKVGLSDAFVYVHRTTQQIPNVRRTIY 302
 QY 279 EYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDY 338
 Db 303 EYHVELQMSKITNISAVEMTPTCLQFNGCGPCVSSQIGFNCWSKLRQCSGFDH 362
 QY 339 ROEMWYDCAQAEAG--RMCEDFQDEHDSASPDTSFSPYDGLTTS----SSLFIDSL 392
 Db 363 RQWVDSCGPEEVQSKMKCEKTEPGTTSQTTSHTTMOFRVLTTRRAVTSQMPSTL 422
 QY 393 TTEDDTKLNYPAGGDLQ--NLSPKTKGTPVHLGTVIGVLAIVLVAAILAGIYINGHP 451
 Db 423 PTEDDTKIALHLKDSGASTDSDSAEKKGGTLAGLIVLILVLIITAAAILVTVMYVHHP 482
 QY 452 TSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMARQC 500
 Db 483 TSAASIFFIERRPSPKAMKFRSGHPAYAEVPGV-EKEGFIVSEQ 530

RESULT 7

Q96E59 ID Q96E59 PRELIMINARY; PRT; 480 AA.
 AC Q96E59;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to RIKEN cDNA 1200007L24 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012885; AAH12885.1; -
DR InterPro: IPR002165; Plexin_repeat.
DR Pfam: PF01437; PSI; 1.
SQ SEQUENCE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 41.9%; Score 1127.5; DB 4; Length 480;
Best Local Similarity 52.6%; Pred. No. 3.3e-92;
Matches 229; Conservative 67; Mismatches 104; Indels 35; Gaps 8;

QY 73 AMDTLPDNRTRVEDHNSYVRLYGPSEPHS-RELWVDVAEAPNSQVKIHTILSNTHRQ 131
DB 74 AVDT---NRASVGDS-----PEPRSFDTLLDDGDNNNTQIE----- 108
QY 132 ASRVLSDFDPYGHPLRQIATIGFTFMGDVTHRMILTATQYVAPLMANFNPGYSDNST 191
DB 109 --RVNLSDFDPYGHFLREITVAIGFYITGEVVRMLTATQYIAPLMANFDPVSRRNST 166
QY 192 VYFONGTVVQWHDVYVQLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 251
DB 167 VRYFONGTALVQWHDVHVLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVQISSTNHP 226
QY 252 VKTGLSDAFMILNPSDPVPESRRSIFEVHRIELDPKSVTMSAVEFTPLPTCLQHRSCD 311
DB 227 VKVGLSDAFVWVVRITQIPNRRRTIYEVHVELQMSKITNISAVEMTPLPTCLQFNRCG 286
QY 312 ACMSSDLTFCNSCHWVLCRCSSGFDYRQEWMDYCAQEAEGRCMEDFQDEHDHDSASDPT 371
DB 287 PCVSSQIGFNCSCWCKLQRCSSGFDYRQWDVSCGPEESKCMCENTEPVETSSRTTIT 346
QY 372 --SFSPYDGLTTS---SSLFDSLTETDDTKLPYAGGDLQ--NNLSPTKGTGPHVHG 425
DB 347 VGATTTFQFVLTTRAVTSQPTSLPTEDDTKIALHLKDNAGASDSDAAEKKGGTLHAG 406
QY 426 TIVGIVLAVLLAAITLAGIYINGHTPSNAALFFTERPHHPAMKFRSHDPDHSYAEVE 485
DB 407 LIIGILVILVATALLVTVYMHHTPSAASIFFIERPSRPAMKFRSGHGPAYAEVE 466
QY 486 PSHEKEGFEAEQ 500
DB 467 PVG-EKEGFIQSEQ 480

RESULT 8
Q9W2V9 PRELIMINARY; PRT; 625 AA.
AC Q9W2V9
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG2221 protein (L040707p).
GN CG2221.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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Db 505 TNTSTSSSGSTPVTPEPSVMSTRAPHATAYIKPGVDHSSDIHADGKVGNAELSKAEADNK 564
 QY 423 HLGTVIGIVLAVLLAAIILAGIYINGHPTSNAALFFIERRPHHW 467
 Db 565 NVGVAEGFVMPICLVFAVTLWLFYARNPHTKSGQLLIQFRESOW 609

RESULT 9

Q18500 ID Q18500 PRELIMINARY; PRT; 476 AA.
 AC Q18500;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE C3688.3 protein.
 GN C3688.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J., Barlow K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z35597; CA84646.1; -;
 SQ SEQUENCE 476 AA; 53918 MW; AC72884A06D57F4D CRC64;

Query Match 22.7%; Score 611; DB 5; Length 476;
 Best Local Similarity 34.2%; Pred. No. 5.4e-46;
 Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;

QY 46 RRARESPGHVSEPPORTQLS-----QDLGGGTAMDITLPDNRTRVVDNHSYYSRLVGPS 100
 Db 62 RTARAAP-----IPKRLASEQEDEEDIPATATIP--PDVEVKNDMDIHQYQAEVTD 115
 QY 101 EPHRELVDVVAEANRSOVKI-----HTILSNTHQASRVLSDFPFYGHPLRQITATG 156
 Db 116 GETLKKYINVEQFMKPKAVGNTSHPLLSQSYRRVARGARLQFKFPYGHKMSMLTATG 175
 QY 157 GFIFMGDVIHRLTATQVAPIMANFPGYSDNSTVYVFDNGTVFVYVQWDHVLQGWEDK 216
 Db 176 GFIVIGDHSNWLAAATQVIAPLMANFHT-YLNNSNIVVADDDGELFVVEWRNVQLKEDKDE 234
 QY 217 GSFTFOAALHDGRIVFAYKEIPMSVPEISSQHPVKTLGLSDAFMILN--PSPDVPESRR 274
 Db 235 HSFTFQTLHKGDLVFIYKDVDPVDNISDANHEVVLKIGISDAYMFKNHLHQAAVP---K 291
 QY 275 RSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDACMSDLT-FNCWSCHVQLR--- 330
 Db 292 RVVIEYHRIEIAAQKIVSNTVILKAQPTCISDPTCDTCTNATLPHFNCWLCHKASHGG 351
 QY 331 --CS--SGFDYRQWMDYGAQBAEGRMCE-DFQDEHDHAS--PDTSFSPYDGLTTTS 384
 Db 352 PFCDEAGLHRRRHOHFWEGNCGYQRSKALYCDADDEDEYDEYDPSQLMPNGGH---TV 408
 QY 385 SSLFIDSITTEDDTKLNPYAGGDCGLQNNLSPKTKGTVPVHLGTIVGLVALLVAAIILAG 444
 Db 409 LPLQADNMKTKDTKTTSEDSDEWKHKKEPK-----GG 442
 QY 445 IYINGHP--TSNAALF 458
 Db 443 VATTAPVGTSSQATF 458

RESULT 10

Q96S09 ID Q96S09 PRELIMINARY; PRT; 151 AA.
 AC Q96S09;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CDNA FLJ14623 fis, clone NT2RP2000173.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saiko K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027529; BAB55178.1; -;
 SQ SEQUENCE 151 AA; 16423 MW; F261A41CC9408347 CRC64;

Query Match 11.1%; Score 297.5; DB 4; Length 151;
 Best Local Similarity 46.1%; Pred. No. 1.1e-18;
 Matches 70; Conservative 24; Mismatches 51; Indels 7; Gaps 4;

QY 355 MCEDFODEDHDSASPD--SFSPYDGLTTTS---SSLFIDSITTEDDTKLNPYAGGDL 409
 Db 1 MCENTEPVEISSRRTTTTGATTTQFRVLTTRAVTSQFPTSLPTEDDTKIALHUKDGA 60
 QY 410 Q-NNLSPKTKGTPVHLGTIVGLVALLVAAIILAGIYINGHPTSNAALFFIERRPHHP 468
 Db 61 STDDSAAEKKGGTLHAGLVILILVIVATLVVYVYHHTSASIFFIERRPSRWP 120
 QY 469 AMKFRSHPDHSIYAEVPSGHEKEGFMEAEQC 500
 Db 121 AMKFRGSGHPAYAEVPGV-EKEGFIVSEQ 151

RESULT 11

ID Q04901 ID Q04901 PRELIMINARY; PRT; 1161 AA.
 AC Q04901;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Entactin/nidogen.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE.
 RX MEDLINE=93238676; PubMed=8477687;
 RA Nakae H., Sugano M., Ishimori Y., Endo T., Obinata T.;
 RT "Ascidian entactin/nidogen: Implication of evolution by shuffling two
 RT kinds of cysteine-rich motifs.";
 RL Eur. J. Biochem. 213:11-19(1993).
 DR EMBL: D14038; BAA03127.1; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000033; Ldl_receptor_rep.
 DR InterPro; IPR003886; Nidogen_ext.
 DR InterPro; IPR000716; Thyroglobulin_1.
 DR InterPro; IPR000834; Zn_carbopept.
 DR Pfam; PF00058; ldl_recept_b; 4.
 DR Pfam; PF00086; thyroglobulin_1; 3.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00135; LY; 4.
 DR SMART; SM00539; NIDO; 1.
 DR SMART; SM00211; TY; 3.


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Db 461 CSECLTA-TDPCGCHSLQRCTFGDCVHSENLENWLDI-----SSGAKCKPKIQIIRSS 515
QY 362 EDHDSASPDTSFSP 375
Db 516 KEKTTVTWVGSFSP 529

RESULT 14
Q9UN95
ID Q9UN95 PRELIMINARY; PRT; 366 AA.
AC Q9UN95;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Mucin 3 (Fragment).
GN MUC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON MUCOSA;
RX MEDLINE=99335363; PubMed=10405327;
RA Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McGuckin M.A.;
RT "The MUC3 gene encodes a transmembrane mucin and is alternatively
RT spliced.";
RL Biochem. Biophys. Res. Commun. 261:83-89(1999).
DR EMBL; AF143371; AAD45882.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00024; SEA; 1.
KW EGF-like domain; Glycoprotein.
FT NON_TER
FT SEQUENCE 366 AA; 40953 MW; 88F3F0E3F439A3C2 CRC64;

Query Match 4.1%; Score 111.5; DB 4; Length 366;
Best Local Similarity 25.0%; Pred. No. 0.18;
Matches 49; Conservative 28; Mismatches 98; Indels 21; Gaps 9;

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QY 182 FNPQYSDNSTVYFDNGTVFVQWDHVV--LQGWEDKGSFTFQAALHHDGRIVFAY---K 236
Db 77 FSPDLNDNTSQAYRDNKTFWQMKIFADMQGFTFKG---VEILSLRNGSIVVDYLVLL 133
QY 237 EIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTMSAV 296
Db 134 EMPFS-POLESEYEQVKTTLKEG--LQNASQDVNSCDSQTLCF---KPDSEIKVNNNSKT 187
QY 297 EFTPLPTCLQHRSCDACMSDDLTF---NCSWCHVLRCSGDFRQRYQEWMDYGCQAEAG 353
Db 188 ELTPAAIC---RRAAPTGYEEFYFPLVEATRLRCVTKCTSGVDN-AIDCHQGCQVLETSG 243
QY 354 RMCEDFQDEHDSASP 369
Db 244 PTCRCYSTDTTHWFSGP 259

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RESULT 15
Q9H3Q6
ID Q9H3Q6 PRELIMINARY; PRT; 877 AA.
AC Q9H3Q6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Intestinal mucin (fragment).
GN MUC3A.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=21183349; PubMed=11289722;
RA Kyo K., Muto T., Nagawa H., Lathrop GM., Nakamura Y.;
RT "Associations of distinct variants of the intestinal mucin gene MUC3A
RT with ulcerative colitis and Crohn's disease.";
RL J. Hum. Genet. 46:5-20(2001).
DR EMBL; AB038784; BAB12118.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00024; SEA; 1.
FT NON_TER
FT SEQUENCE 877 AA; 93720 MW; 09BE5E86BC838DFA CRC64;

Query Match 4.1%; Score 111.5; DB 4; Length 877;
Best Local Similarity 25.0%; Pred. No. 0.65;
Matches 49; Conservative 28; Mismatches 98; Indels 21; Gaps 9;

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Search completed: April 22, 2003, 16:07:49
Job time : 37 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 16:14:16 ; Search time 90 Seconds
(without alignments)
1144.706 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

Sequence: 1 MRGELWLLVLRREARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	500	100.0	500	4	Q9HCT9		Q9HCT9 homo sapien
2	35	7.0	500	11	Q9CWW5		Q9CWW5 mus musculus
3	35	7.0	500	11	Q91ZV7		Q91ZV7 mus musculus
4	10	2.0	480	4	Q96E59		Q96E59 homo sapien
5	10	2.0	529	4	Q96PD9		Q96PD9 homo sapien
6	10	2.0	530	11	Q9DC11		Q9DC11 mus musculus
7	10	2.0	530	11	Q91ZV6		Q91ZV6 mus musculus
8	9	1.8	655	16	P94476		P94476 bacillus su
9	8	1.6	208	17	Q97019		Q97019 sulfolobus
10	8	1.6	224	16	Q9S2F8		Q9S2F8 streptomyce
11	8	1.6	317	2	Q54303		Q54303 streptomyce
12	8	1.6	363	17	Q9HQA6		Q9HQA6 halobacteri
13	8	1.6	429	16	Q9AC73		Q9AC73 staphylococ
14	8	1.6	472	16	Q9JYC8		Q9JYC8 neisseria m
15	8	1.6	472	16	Q9JTB1		Q9JTB1 neisseria m
16	8	1.6	476	5	Q18500		Q18500 caenorhabdi

17	1.6	483	16	054179	054179 streptomyce
18	1.6	510	16	Q3L1B4	Q3L1B4 streptomyce
19	1.6	519	2	033968	033968 streptomyce
20	1.6	562	16	Q8YKQ2	Q8YKQ2 anabaena sp
21	1.6	625	5	Q9W2V9	Q9W2V9 drosophila
22	1.6	751	2	Q9ZA45	Q9ZA45 streptomyce
23	1.6	924	4	094958	094958 homo sapien
24	1.6	1136	17	Q970E1	Q970E1 sulfolobus
25	1.4	68	6	P79120	P79120 bos taurus
26	1.4	79	5	Q9NM35	Q9NM35 leishmania
27	1.4	82	16	Q92IE9	Q92IE9 rickettsia
28	1.4	90	16	Q9K3G8	Q9K3G8 streptomyce
29	1.4	93	2	Q48852	Q48852 lactobacilli
30	1.4	100	2	054389	054389 streptomyce
31	1.4	103	8	Q9GBP6	Q9GBP6 inversidens
32	1.4	103	8	Q9GBP4	Q9GBP4 inversidens
33	1.4	103	8	Q9GBP3	Q9GBP3 lanceolaria
34	1.4	103	8	Q9GBP1	Q9GBP1 anodonta wo
35	1.4	114	17	052012	052012 halobacteri
36	1.4	116	16	Q985J4	Q985J4 rhizobium 1
37	1.4	122	2	P94859	P94859 klebsiella
38	1.4	124	12	Q8QKV6	Q8QKV6 ectocarpus
39	1.4	133	10	Q9LE71	Q9LE71 oryza sativ
40	1.4	133	16	Q87GJ8	Q87GJ8 clostridium
41	1.4	147	16	Q8Z948	Q8Z948 salmonella
42	1.4	150	16	Q9A4T0	Q9A4T0 caulobacter
43	1.4	151	4	Q96SU9	Q96SU9 homo sapien
44	1.4	151	8	Q9G0I9	Q9G0I9 quincuncina
45	1.4	151	8	Q9G0I8	Q9G0I8 fusconala s
46	1.4	151	8	Q9G0I7	Q9G0I7 quincuncina
47	1.4	151	8	Q9G0I6	Q9G0I6 obovaria ro
48	1.4	151	8	Q9G0K4	Q9G0K4 quincuncina
49	1.4	151	8	Q9G0K3	Q9G0K3 quincuncina
50	1.4	151	8	Q9G0K2	Q9G0K2 quincuncina
51	1.4	151	8	Q9G0K0	Q9G0K0 obovaria un
52	1.4	151	8	Q9G0J9	Q9G0J9 obovaria ol
53	1.4	151	8	Q9G0J8	Q9G0J8 fusconala e
54	1.4	151	8	Q9G0J5	Q9G0J5 fusconala f
55	1.4	151	8	Q9G0J3	Q9G0J3 anodonta cy
56	1.4	151	8	Q9G0J2	Q9G0J2 cumberlandi
57	1.4	154	16	Q8YE01	Q8YE01 bruceella me
58	1.4	164	17	Q8TLA6	Q8TLA6 methanosarc
59	1.4	166	16	Q97I03	Q97I03 clostridium
60	1.4	170	2	Q9AQM6	Q9AQM6 pseudomonas
61	1.4	170	16	Q9A743	Q9A743 caulobacter
62	1.4	172	4	Q9NPA9	Q9NPA9 homo sapien
63	1.4	175	17	Q8ZWM1	Q8ZWM1 pyrobaculum
64	1.4	177	9	Q94MQ1	Q94MQ1 bacterioph
65	1.4	177	16	Q9A4J3	Q9A4J3 caulobacter
66	1.4	178	5	Q9Y0W0	Q9Y0W0 schistocerc
67	1.4	178	16	Q9RT80	Q9RT80 deinococcus
68	1.4	183	12	Q9J3P3	Q9J3P3 avian infec
69	1.4	183	12	Q9J3P2	Q9J3P2 avian infec
70	1.4	183	12	Q9J3P1	Q9J3P1 avian infec
71	1.4	183	12	Q9J3P0	Q9J3P0 avian infec
72	1.4	183	12	Q9J3N9	Q9J3N9 avian infec
73	1.4	183	12	Q9J3N8	Q9J3N8 avian infec
74	1.4	186	16	Q8UIJ1	Q8UIJ1 agrobacteri
75	1.4	189	5	Q95SV0	Q95SV0 drosophila
76	1.4	194	8	Q9ME60	Q9ME60 alasmidonta
77	1.4	194	8	Q9MQV0	Q9MQV0 strophotus
78	1.4	195	8	Q9MQU5	Q9MQU5 lasmignona c
79	1.4	195	8	Q9MQU4	Q9MQU4 lasmignona c
80	1.4	195	11	Q9CSC7	Q9CSC7 mus musculus
81	1.4	196	2	Q8RQT0	Q8RQT0 uncultured
82	1.4	197	8	Q8WCR7	Q8WCR7 lampsillis p
83	1.4	197	8	Q8WCR4	Q8WCR4 lampsillis a
84	1.4	197	8	Q8WCR3	Q8WCR3 lampsillis a
85	1.4	197	8	Q8WCR2	Q8WCR2 lampsillis s
86	1.4	197	8	Q8WCR1	Q8WCR1 lampsillis s
87	1.4	197	8	Q8WCR0	Q8WCR0 lampsillis s
88	1.4	197	8	Q8WCQ9	Q8WCQ9 lampsillis a
89	1.4	197	8	Q8WCQ7	Q8WCQ7 lampsillis a

90	7	1.4	197	8	Q8WC66	Q8wcq6 lampisilis a	163	7	1.4	223	12	Q91NK5	Q91nk5 avian infec
91	7	1.4	197	8	Q8WCQ2	Q8wcq2 lampisilis o	164	7	1.4	223	12	Q91NK4	Q91nk4 avian infec
92	7	1.4	197	8	Q8WCQ0	Q8wcq0 obliquaria	165	7	1.4	223	12	Q91OE2	Q91oe2 avian infec
93	7	1.4	197	8	Q8W8J1	Q8w8j1 lampisilis a	166	7	1.4	223	14	P97967	P97967 unidentified
94	7	1.4	197	8	Q8W8J0	Q8w8j0 lampisilis p	167	7	1.4	224	16	Q986K0	Q986k0 rhizobium l
95	7	1.4	199	8	Q89512	Q89512 lampisilis o	168	7	1.4	225	12	Q9J4A6	Q9j4a6 avian infec
96	7	1.4	199	8	Q89513	Q89513 obliquaria	169	7	1.4	225	12	Q9J4B3	Q9j4b3 avian infec
97	7	1.4	202	5	Q9N9A7	Q9n9a7 leishmania	170	7	1.4	225	12	Q99AS5	Q99as5 avian infec
98	7	1.4	204	2	Q8RQ57	Q8rq57 uncultured	171	7	1.4	225	12	Q91SA1	Q91sa1 avian infec
99	7	1.4	204	8	Q33836	Q33836 amblema pli	172	7	1.4	225	12	Q91SA0	Q91sa0 avian infec
100	7	1.4	204	8	Q33685	Q33685 anodonta cy	173	7	1.4	225	12	Q91S99	Q91s99 avian infec
101	7	1.4	204	8	Q35084	Q35084 mutela rost	174	7	1.4	225	12	Q91S98	Q91s98 avian infec
102	7	1.4	205	17	Q8Z0F7	Q8zuf7 pyrobaculum	175	7	1.4	225	12	Q91GB7	Q91gb7 avian infec
103	7	1.4	206	12	Q82614	Q82614 avian infec	176	7	1.4	225	12	Q910H8	Q910h8 avian infec
104	7	1.4	208	8	Q8SFU0	Q8sfu0 pseudanodon	177	7	1.4	226	12	Q9J0X1	Q9j0x1 avian infec
105	7	1.4	209	2	P94796	P94796 francisella	178	7	1.4	230	16	Q8U0H6	Q8u0h6 agrobacteri
106	7	1.4	209	8	Q8SK63	Q8sk63 unio tumidu	179	7	1.4	234	4	Q9H5C5	Q9h5c5 homo sapien
107	7	1.4	210	8	Q94R01	Q94r01 glebula rot	180	7	1.4	235	8	Q956B4	Q956b4 anodonta wo
108	7	1.4	210	8	Q94R00	Q94r00 actinonaias	181	7	1.4	242	6	Q9BFG2	Q9bfg2 talpa alta
109	7	1.4	210	8	Q94Q28	Q94q28 unio tumidu	182	7	1.4	243	5	Q95T03	Q95t03 drosophila
110	7	1.4	210	8	Q94Q27	Q94q27 fusconala f	183	7	1.4	247	5	O16379	O16379 caenorhabdi
111	7	1.4	211	8	Q94Q26	Q94q26 pyganodon g	184	7	1.4	248	16	Q92KD6	Q92kd6 rhizobium m
112	7	1.4	210	8	Q94Q25	Q94q25 coelatura a	185	7	1.4	251	2	Q9EV39	Q9ev39 streptococc
113	7	1.4	210	8	Q94Q23	Q94q23 mutela dubi	186	7	1.4	254	16	Q9X936	Q9x936 streptomyc
114	7	1.4	210	8	Q94Q20	Q94q20 strophitus	187	7	1.4	260	5	Q9VPH2	Q9veh2 drosophila
115	7	1.4	210	8	Q94QY5	Q94qy5 monocondyla	188	7	1.4	260	16	Q92W83	Q92w83 rhizobium m
116	7	1.4	210	8	Q94QY1	Q94qy1 cyrtionalas	189	7	1.4	271	16	Q9X130	Q9x130 thermotoga
117	7	1.4	210	8	Q94QX9	Q94qx9 elliptio di	190	7	1.4	278	2	Q9A152	Q9a152 burkholderi
118	7	1.4	210	8	Q94QX7	Q94qx7 cumberlandi	191	7	1.4	282	3	Q12057	Q12057 saccharomyc
119	7	1.4	210	8	Q94QX6	Q94qx6 pleurobema	192	7	1.4	293	2	O50269	O50269 agrobacteri
120	7	1.4	210	8	Q94QX5	Q94qx5 gonidea ang	193	7	1.4	294	17	Q8TQJ7	Q8tqj7 methanosarc
121	7	1.4	210	8	Q94QX4	Q94qx4 toxolasma l	194	7	1.4	295	16	Q930C6	Q930c6 rhizobium m
122	7	1.4	210	8	Q94QX3	Q94qx3 quadrula qu	195	7	1.4	301	6	Q9BFE6	Q9bfe6 tarsius ban
123	7	1.4	213	4	Q9Y4U6	Q9y4u6 homo sapien	196	7	1.4	304	10	Q9LPL2	Q9lp12 arabidopsis
124	7	1.4	213	4	Q9U0N3	Q9u0n3 homo sapien	197	7	1.4	310	4	O75938	O75938 homo sapien
125	7	1.4	214	16	Q92R50	Q92r50 rhizobium m	198	7	1.4	312	16	Q9ZBG0	Q9zbg0 streptomyc
126	7	1.4	215	8	Q9XMW4	Q9xmw4 fusconala f	199	7	1.4	318	2	Q93F49	Q93f49 pseudomonas
127	7	1.4	215	8	Q9XNV8	Q9xnv8 actinonaias	200	7	1.4	318	16	Q8VCJ2	Q8vcj2 brucella me
128	7	1.4	215	8	Q8WB66	Q8wb66 anodonta cy	201	7	1.4	321	16	Q916G4	Q916g4 pseudomonas
129	7	1.4	215	14	P97975	P97975 unidentified	202	7	1.4	322	16	Q9RK51	Q9rk51 streptomyc
130	7	1.4	216	8	Q9XK72	Q9xk72 cumberlandi	203	7	1.4	323	16	Q9XPX0	Q9xp00 raistonias s
131	7	1.4	216	8	Q9XK71	Q9xk71 elliptio di	204	7	1.4	327	16	Q49822	Q49822 mycobacteri
132	7	1.4	216	8	Q9XK23	Q9xk23 pleurobema	205	7	1.4	328	6	Q9BFE4	Q9bfc4 manis penta
133	7	1.4	216	8	Q9XMW8	Q9xmw8 alasmidonta	206	7	1.4	329	6	Q9BFE1	Q9bfe1 artibeus ja
134	7	1.4	216	8	Q9XMW7	Q9xmw7 lasmigona c	207	7	1.4	329	6	Q9BFD8	Q9bfd8 nycteris th
135	7	1.4	216	8	Q9XMW6	Q9xmw6 pyganodon g	208	7	1.4	329	11	Q99NT8	Q99nt8 dipodomys h
136	7	1.4	216	8	Q9XMW5	Q9xmw5 strophitus	209	7	1.4	330	5	Q9BHW8	Q9bmw8 trypanosoma
137	7	1.4	216	8	Q9XMW3	Q9xmw3 quadrula qu	210	7	1.4	330	6	Q9BFG8	Q9bfg8 choleopus h
138	7	1.4	216	8	Q9TFB1	Q9tfb1 amblema pli	211	7	1.4	330	6	Q9BFG7	Q9bfq7 choleopus d
139	7	1.4	216	8	Q9XMW0	Q9xmw0 ligumia nas	212	7	1.4	330	6	Q9BFG6	Q9bfg6 euphractus
140	7	1.4	216	8	Q9XNV7	Q9xnv7 lampisilis c	213	7	1.4	330	6	Q9BFG5	Q9bfg5 chaetophrac
141	7	1.4	216	8	Q9XNV6	Q9xnv6 lampisilis c	214	7	1.4	330	6	Q9BFG4	Q9bfg4 tamandua te
142	7	1.4	216	8	Q9XNV5	Q9xnv5 lampisilis f	215	7	1.4	330	6	Q9BFG3	Q9bfg3 myrmecophag
143	7	1.4	216	8	Q9XMV4	Q9xmv4 villosa van	216	7	1.4	330	6	Q9BFG0	Q9bfg0 soxex arane
144	7	1.4	216	8	Q9TFB0	Q9tfb0 villosa van	217	7	1.4	330	6	Q9BFF8	Q9bff8 trichechus
145	7	1.4	217	5	Q23973	Q23973 drosophila	218	7	1.4	330	6	Q9BFF7	Q9bff7 procavia ca
146	7	1.4	217	5	Q9VSJ7	Q9vsj7 drosophila	219	7	1.4	330	6	Q9BFF6	Q9bff6 loxodonta a
147	7	1.4	219	6	Q9BFF9	Q9bff9 echinops te	220	7	1.4	330	6	Q9BFF5	Q9bff5 macroscelid
148	7	1.4	219	16	Q98P47	Q98p47 rhizobium l	221	7	1.4	330	6	Q9BFF4	Q9bff4 elephantu
149	7	1.4	220	2	Q9RQ01	Q9rq01 staphylococ	222	7	1.4	330	6	Q9BFF1	Q9bff1 syvillagus
150	7	1.4	220	6	Q9BFF2	Q9bff2 tragelaphus	223	7	1.4	330	6	Q9BFF0	Q9bff0 ochotona hy
151	7	1.4	220	16	Q99QX4	Q99qx4 staphylococ	224	7	1.4	330	6	Q9BFE8	Q9bfe8 tupaia mino
152	7	1.4	221	6	Q9BFF3	Q9bff3 orycteropus	225	7	1.4	330	6	Q9BFE7	Q9bfe7 lemur catia
153	7	1.4	221	6	Q9BFE9	Q9bfe9 cynocephalu	226	7	1.4	330	6	Q9BFE6	Q9bfe6 pteropopus gi
154	7	1.4	221	11	Q99NT7	Q99nt7 heteroceph	227	7	1.4	330	6	Q9BFE0	Q9bfe0 roussetus l
155	7	1.4	221	11	Q99NT6	Q99nt6 cavia tschu	228	7	1.4	330	6	Q9BFD9	Q9bfd9 megatera n
156	7	1.4	222	6	Q9BFG9	Q9bfg9 didelphis m	229	7	1.4	330	6	Q9BFD7	Q9bfd7 tursiops tr
157	7	1.4	223	8	Q8WEU0	Q8weu0 lampisilis c	230	7	1.4	330	6	Q9BFD6	Q9bfd6 hippopotam
158	7	1.4	223	12	Q91SA4	Q9lsa4 avian infec	231	7	1.4	330	6	Q9BFD5	Q9bfd5 lama glama
159	7	1.4	223	12	Q91SA3	Q9lsa3 avian infec	232	7	1.4	330	6	Q9BFD4	Q9bfd4 sus scrofa
160	7	1.4	223	12	Q91S96	Q9ls96 avian infec	233	7	1.4	330	6	Q9BFD3	Q9bfd3 equus cabal
161	7	1.4	223	12	Q91S95	Q9ls95 avian infec	234	7	1.4	330	6	Q9BFD2	Q9bfd2 okapia john
162	7	1.4	223	12	Q91NK6	Q91nk6 avian infec	235	7	1.4	330	6	Q9BFD1	Q9bfd1 ceratotheri

236	7	1.4	330	6	Q9BFC9	Q9bfc9 tapirus ind	309	7	1.4	463	4	Q9H9V9	Q9h9v9 homo sapien
237	7	1.4	330	6	Q9BFC8	Q9bfc8 felis silve	310	7	1.4	463	5	Q93WX6	Q93wx6 arabisdopsis
238	7	1.4	330	6	Q9BFC7	Q9bfc7 leopardus p	311	7	1.4	469	5	O44321	O44321 tenebrio mo
239	7	1.4	330	6	Q9BFC6	Q9bfc6 panthera on	312	7	1.4	469	5	Q20752	Q20752 caenorhabdi
240	7	1.4	330	6	Q9BFC5	Q9bfc5 canis famil	313	7	1.4	469	16	Q915N9	Q915n9 pseudomonas
241	7	1.4	330	11	Q99NU6	Q99nu6 castor cana	314	7	1.4	470	2	Q60154	Q60154 peobacter
242	7	1.4	330	11	Q99NU5	Q99nu5 muscardinus	315	7	1.4	471	11	Q35162	Q35162 rattus norv
243	7	1.4	330	11	Q99NU4	Q99nu4 pedetes cap	316	7	1.4	488	5	Q18760	Q18760 caenorhabdi
244	7	1.4	330	11	Q99NU0	Q99nu0 hystrix bra	317	7	1.4	497	16	Q98B98	Q98b98 rhizobium l
245	7	1.4	330	11	Q99NT9	Q99nt9 erethizon d	318	7	1.4	498	16	Q82L78	Q82l78 salmonella
246	7	1.4	330	11	Q99NT5	Q99nt5 hydrochoeru	319	7	1.4	498	16	Q822C9	Q822c9 salmonella
247	7	1.4	330	11	Q99NT4	Q99nt4 myocastor c	320	7	1.4	506	16	Q9K0Q3	Q9k0q3 neisseria m
248	7	1.4	330	11	Q99NT3	Q99nt3 agouti tacz	321	7	1.4	506	16	Q9JVT2	Q9jvt2 neisseria m
249	7	1.4	331	6	Q9BFC1	Q9bfc1 condylura c	322	7	1.4	512	8	Q956C8	Q956c8 inversidens
250	7	1.4	331	11	Q99NU7	Q99nu7 tamias stri	323	7	1.4	519	10	Q9FJ09	Q9fj09 arabisdopsis
251	7	1.4	331	11	Q99NU3	Q99nu3 mus musculu	324	7	1.4	520	10	Q9SLD2	Q9slld2 arabisdopsis
252	7	1.4	331	11	Q99NU2	Q99nu2 rattus norv	325	7	1.4	525	16	Q9K634	Q9k634 bacillus ha
253	7	1.4	331	11	Q99NU1	Q99nu1 cricetus	326	7	1.4	525	16	Q9K0Q3	Q9k0q3 neisseria m
254	7	1.4	333	16	Q97ER9	Q97er9 clostridium	327	7	1.4	526	10	Q9SJE3	Q9sje3 arabisdopsis
255	7	1.4	336	16	Q8YUV2	Q8yuv2 anabaena sp	328	7	1.4	528	5	Q9VTO8	Q9vtq8 drosophila
256	7	1.4	338	16	Q8YV187	Q8yvl87 brucella me	329	7	1.4	533	2	Q93NX3	Q93nx3 streptomyce
257	7	1.4	340	5	Q9VNL5	Q9vnl5 drosophila	330	7	1.4	535	9	Q9WBL8	Q9wbl8 corynephage
258	7	1.4	346	16	Q8ZDS8	Q8zds8 yersinia pe	331	7	1.4	541	16	Q91493	Q91493 pseudomonas
259	7	1.4	346	16	Q8YCU5	Q8ycu5 brucella me	332	7	1.4	542	12	Q92377	Q92377 bombyx mori
260	7	1.4	347	16	Q92XA5	Q92xa5 rhizobium m	333	7	1.4	557	10	Q8RWK1	Q8rwl1 arabisdopsis
261	7	1.4	352	16	Q97KT1	Q97kt1 clostridium	334	7	1.4	569	10	Q9FP06	Q9fp06 oryza sativ
262	7	1.4	358	9	Q9FZT1	Q9fzt1 pseudomonas	335	7	1.4	574	2	Q9AQH1	Q9aqh1 pseudomonas
263	7	1.4	365	15	Q97R80	Q97r80 human immun	336	7	1.4	574	16	Q9HWG7	Q9hwg7 pseudomonas
264	7	1.4	365	16	Q92T69	Q92t69 rhizobium m	337	7	1.4	592	16	Q67937	Q67937 aquifex aeo
265	7	1.4	370	11	Q9DCX3	Q9dcx3 mus musculu	338	7	1.4	599	6	O19112	O19112 sus scrofa
266	7	1.4	372	2	Q54025	Q54025 salmonella	339	7	1.4	609	5	Q22680	Q22680 caenorhabdi
267	7	1.4	372	2	Q54026	Q54026 salmonella	340	7	1.4	614	5	Q9W3P8	Q9w3p8 drosophila
268	7	1.4	372	2	Q54027	Q54027 salmonella	341	7	1.4	623	17	Q971X1	Q971x1 sulfolobus
269	7	1.4	372	2	Q54028	Q54028 salmonella	342	7	1.4	626	16	Q9KYP5	Q9kyp5 streptomyce
270	7	1.4	372	2	Q54029	Q54029 salmonella	343	7	1.4	627	16	Q98PG2	Q98pg2 mycoplasma
271	7	1.4	372	2	Q54030	Q54030 salmonella	344	7	1.4	630	1	Q93675	Q93675 sulfolobus
272	7	1.4	372	2	Q54031	Q54031 salmonella	345	7	1.4	643	16	Q9KMQ2	Q9kmq2 vibrio chol
273	7	1.4	372	2	Q54032	Q54032 salmonella	346	7	1.4	648	17	Q8TH20	Q8th20 methanosarc
274	7	1.4	372	2	Q54037	Q54037 salmonella	347	7	1.4	653	16	Q9RDB5	Q9rdb5 streptomyce
275	7	1.4	372	2	Q54038	Q54038 salmonella	348	7	1.4	662	4	Q9UPF7	Q9upf7 homo sapien
276	7	1.4	372	2	Q54039	Q54039 salmonella	349	7	1.4	680	10	Q8W0I8	Q8w0i8 oryza sativ
277	7	1.4	372	2	Q54040	Q54040 salmonella	350	7	1.4	693	3	Q00141	Q00141 aspergillus
278	7	1.4	372	2	Q56052	Q56052 salmonella	351	7	1.4	723	16	Q8YD09	Q8yd09 brucella me
279	7	1.4	372	2	Q57178	Q57178 salmonella	352	7	1.4	731	10	Q9AKD1	Q9akd1 arabisdopsis
280	7	1.4	372	2	Q54034	Q54034 salmonella	353	7	1.4	745	13	Q9PVS3	Q9pvs3 cyprinus ca
281	7	1.4	372	2	Q54036	Q54036 salmonella	354	7	1.4	751	10	O48802	O48802 arabisdopsis
282	7	1.4	372	16	Q8Z490	Q8z490 salmonella	355	7	1.4	754	5	Q8SXJ1	Q8sxj1 drosophila
283	7	1.4	374	16	Q92U19	Q92uy9 rhizobium m	356	7	1.4	763	10	Q9FZ11	Q9fz11 arabisdopsis
284	7	1.4	376	11	Q92Z24	Q92z24 rattus norv	357	7	1.4	769	16	Q97IS9	Q97is9 clostridium
285	7	1.4	379	16	Q92SB1	Q92sb1 rhizobium m	358	7	1.4	773	16	Q97J97	Q97j97 clostridium
286	7	1.4	382	2	Q9RHC3	Q9rhc3 bradyrhizob	359	7	1.4	782	10	P92988	P92988 arabisdopsis
287	7	1.4	394	17	Q58179	Q58179 pyrococcus	360	7	1.4	803	4	Q96Q00	Q96q00 homo sapien
288	7	1.4	400	2	Q52293	Q52293 pseudomonas	361	7	1.4	839	17	Q8TQ74	Q8tq74 methanosarc
289	7	1.4	401	4	Q9H970	Q9h970 homo sapien	362	7	1.4	862	16	Q8RES2	Q8res2 fusobacteri
290	7	1.4	402	17	Q97Z99	Q97z99 sulfolobus	363	7	1.4	885	16	Q87658	Q87658 salmonella
291	7	1.4	404	16	Q9JWX3	Q9jwx3 neisseria m	364	7	1.4	891	16	Q82JUC2	Q82juc2 rickettsia
292	7	1.4	416	5	Q96360	Q96360 hyphantria	365	7	1.4	903	12	Q8VBL6	Q8vbl6 powassan vi
293	7	1.4	417	4	Q96EU8	Q96eu8 homo sapien	366	7	1.4	920	5	Q960B9	Q960b9 drosophila
294	7	1.4	417	11	Q92LW7	Q92lw7 cricetus	367	7	1.4	920	5	Q9VBP7	Q9vpb7 drosophila
295	7	1.4	420	16	Q8YU59	Q8yus9 anabaena sp	368	7	1.4	927	16	Q981V0	Q981v0 rhizobium l
296	7	1.4	421	16	Q9EX44	Q9ex44 streptomyce	369	7	1.4	936	5	Q9N910	Q9n910 trypanosoma
297	7	1.4	422	11	Q88298	Q88298 rattus norv	370	7	1.4	950	13	Q9YHC9	Q9ych9 xenopus lae
298	7	1.4	425	16	Q9KZ22	Q9kz22 streptomyce	371	7	1.4	953	16	P73173	P73173 synchocyst
299	7	1.4	430	16	Q97HA1	Q97ha1 clostridium	372	7	1.4	966	5	Q9U3P1	Q9u3p1 caenorhabdi
300	7	1.4	433	2	Q9ZA36	Q9za36 streptomyce	373	7	1.4	967	13	Q57579	Q57579 gallus gall
301	7	1.4	451	16	Q9HYK0	Q9hyk0 pseudomonas	374	7	1.4	999	16	Q9Z517	Q9z517 streptomyce
302	7	1.4	452	3	Q9Y7L5	Q9y7l5 schizosacch	375	7	1.4	1014	6	O62805	O62805 tursoops tr
303	7	1.4	452	5	Q9N196	Q9n196 physarum po	376	7	1.4	1071	16	O69695	O69695 mycobacteri
304	7	1.4	452	11	Q9CXM9	Q9cxm9 mus musculu	377	7	1.4	1092	2	Q54099	Q54099 streptococc
305	7	1.4	454	5	Q9W4S1	Q9w4s1 drosophila	378	7	1.4	1096	16	Q9ABV4	Q9abv4 caulobacter
306	7	1.4	454	5	Q8SZ66	Q8sz66 drosophila	379	7	1.4	1184	4	O75339	O75339 homo sapien
307	7	1.4	456	5	Q17675	Q17675 caenorhabdi	380	7	1.4	1241	4	Q14148	Q14148 homo sapien
308	7	1.4	458	2	Q9FPD17	Q9fpd17 pseudomonas	381	7	1.4	1245	12	O9YVQ9	O9yvq9 ateline her

382	7	1.4	1262	4	075163	075163 homo sapien	455	6	1.2	73	12	091FP8	091FP8 chilo iride
383	7	1.4	1270	10	09L129	09L129 oryza sativ	456	6	1.2	74	2	093CH9	093CH9 bacillus su
384	7	1.4	1298	10	09LSA4	09LSA4 arabidopsis	457	6	1.2	74	6	09N068	09N068 macaca fasc
385	7	1.4	1308	17	09V2G5	09V2G5 pyrococcus	458	6	1.2	74	10	09SDN7	09SDN7 nicotiana t
386	7	1.4	1323	4	096RG2	096RG2 homo sapien	459	6	1.2	74	16	08Y200	08Y200 anabaena sp
387	7	1.4	1421	2	09L8C9	09L8C9 polyanthum	460	6	1.2	77	16	08RDS1	08RDS1 fusobacteri
388	7	1.4	1421	2	09KJ00	09KJ00 polyanthum	461	6	1.2	78	5	003622	003622 plasmodium
389	7	1.4	1505	2	09F0D7	09F0D7 streptomyce	462	6	1.2	78	12	08V717	08V717 smian herp
390	7	1.4	1628	10	09LNE9	09LNE9 arabidopsis	463	6	1.2	78	12	089339	089339 paramecium
391	7	1.4	1698	5	09V5J8	09V5J8 drosophila	464	6	1.2	79	5	0872C7	0872C7 dictyosteli
392	7	1.4	1759	5	09XTP8	09XTP8 plasmodium	465	6	1.2	80	6	095MH4	095MH4 pan troglod
393	7	1.4	1839	2	030765	030765 streptomyce	466	6	1.2	80	6	095MH3	095MH3 gorilla gor
394	7	1.4	1858	12	091PR6	091PR6 squash mosa	467	6	1.2	80	6	095MH2	095MH2 pongo pygma
395	7	1.4	2126	17	08T161	08T161 methanosarc	468	6	1.2	80	6	095MH1	095MH1 papio anubi
396	7	1.4	2188	16	P94996	P94996 mycobacteri	469	6	1.2	80	6	095MH0	095MH0 macaca mule
397	7	1.4	2391	5	027732	027732 plasmodium	470	6	1.2	80	6	095WG9	095WG9 macaca sule
398	7	1.4	3670	16	0924X5	0924X5 streptomyce	471	6	1.2	80	12	0913U4	0913U4 foot-and-mo
399	7	1.4	3944	5	018667	018667 caenorhabdi	472	6	1.2	81	5	09VPK9	09VPK9 drosophila
400	7	1.4	4268	16	08X3F2	08X3F2 raietonia s	473	6	1.2	81	10	09LSW4	09LSW4 arabidopsis
401	6	1.2	15	2	09R4Y0	09R4Y0 pseudomonas	474	6	1.2	82	2	08RP85	08RP85 streptococ
402	6	1.2	20	10	09SBE8	09SBE8 zea mays (m	475	6	1.2	82	12	09Q3H8	09Q3H8 hepatitis c
403	6	1.2	26	2	005605	005605 pseudomonas	476	6	1.2	82	12	09Q3H7	09Q3H7 hepatitis c
404	6	1.2	27	11	035837	035837 rattus sp.	477	6	1.2	82	12	09Q3H6	09Q3H6 hepatitis c
405	6	1.2	28	15	073626	073626 human immun	478	6	1.2	82	15	074089	074089 human immun
406	6	1.2	35	11	09JW75	09JW75 mus musculus	479	6	1.2	83	2	09AQ40	09AQ40 vibrio chol
407	6	1.2	38	11	09ES99	09ES99 rattus norv	480	6	1.2	83	12	09WGP5	09WGP5 human papil
408	6	1.2	43	4	014334	014334 homo sapien	481	6	1.2	83	12	09WGD9	09WGD9 human papil
409	6	1.2	43	4	014362	014362 homo sapien	482	6	1.2	83	12	09W884	09W884 human papil
410	6	1.2	43	11	064720	064720 rattus norv	483	6	1.2	83	16	09ADE4	09ADE4 streptomyce
411	6	1.2	45	12	068590	068590 hepatitis c	484	6	1.2	85	5	09VDM5	09VDM5 drosophila
412	6	1.2	45	12	068591	068591 hepatitis c	485	6	1.2	85	10	09C755	09C755 arabidopsis
413	6	1.2	45	12	068592	068592 hepatitis c	486	6	1.2	87	15	09YXB5	09YXB5 human immun
414	6	1.2	45	12	068602	068602 hepatitis c	487	6	1.2	87	15	09YVC0	09YVC0 human immun
415	6	1.2	45	12	068603	068603 hepatitis c	488	6	1.2	88	2	087566	087566 bacillus ps
416	6	1.2	47	2	047111	047111 escherichia	489	6	1.2	88	16	08Y522	08Y522 listeria mo
417	6	1.2	48	16	099WX4	099WX4 staphylococ	490	6	1.2	88	17	09HNW9	09HNW9 halobacteri
418	6	1.2	52	13	09PMG0	09PMG0 coturnix co	491	6	1.2	89	2	093L81	093L81 bacillus sp
419	6	1.2	55	16	09KVV7	09KVV7 vibrio chol	492	6	1.2	89	2	093L80	093L80 bacillus sp
420	6	1.2	56	17	08TXH4	08TXH4 methanopyru	493	6	1.2	89	2	093L77	093L77 bacillus sp
421	6	1.2	58	15	P82290	P82290 anopheles g	494	6	1.2	89	16	09POT9	09POT9 ureaplasma
422	6	1.2	58	11	09Q0238	09Q0238 mus musculus	495	6	1.2	90	16	09PFS3	09PFS3 xylella fas
423	6	1.2	59	2	09L7E0	09L7E0 synchococc	496	6	1.2	90	5	09VWN6	09VWN6 drosophila
424	6	1.2	60	1	08X244	08X244 haloarcula	497	6	1.2	91	5	09VW03	09VW03 drosophila
425	6	1.2	61	2	09L7D8	09L7D8 synchococc	498	6	1.2	91	17	027563	027563 methanobact
426	6	1.2	60	5	095085	095085 caenorhabdi	499	6	1.2	92	11	091265	091265 sigmodon hi
427	6	1.2	62	16	0935E1	0935E1 salmonella	500	6	1.2	92	12	091FL2	091FL2 chilo iride
428	6	1.2	63	4	09BAX1	09BAX1 homo sapien	501	6	1.2	92	6	09GLK8	09GLK8 oryctolagus
429	6	1.2	66	2	085696	085696 streptomyce	502	6	1.2	93	10	09C6F1	09C6F1 arabidopsis
430	6	1.2	66	16	09EWS5	09EWS5 streptomyce	503	6	1.2	93	16	09RJ49	09RJ49 streptomyce
431	6	1.2	67	2	053997	053997 nodularia s	504	6	1.2	93	17	0972V4	0972V4 sulfolobus
432	6	1.2	67	2	053999	053999 nodularia s	505	6	1.2	94	5	09VTK4	09VTK4 drosophila
433	6	1.2	67	2	054001	054001 nodularia s	506	6	1.2	94	8	094YM4	094YM4 rana nigrom
434	6	1.2	67	2	093E85	093E85 nodularia h	507	6	1.2	94	10	08S3J7	08S3J7 oryza sativ
435	6	1.2	67	2	093E83	093E83 nodularia s	508	6	1.2	94	16	098H94	098H94 rhizobium l
436	6	1.2	67	2	093E82	093E82 nodularia s	509	6	1.2	94	16	08YHS5	08YHS5 bruceella me
437	6	1.2	67	2	093E80	093E80 nodularia b	510	6	1.2	94	17	082ZB9	082ZB9 pyrobaculum
438	6	1.2	67	2	093E78	093E78 nodularia s	511	6	1.2	95	2	09S501	09S501 nodularia s
439	6	1.2	67	2	093E76	093E76 nodularia s	512	6	1.2	95	2	09S429	09S429 nodularia s
440	6	1.2	67	2	093E74	093E74 nodularia s	513	6	1.2	95	2	09S427	09S427 nodularia s
441	6	1.2	67	2	093E72	093E72 nodularia s	514	6	1.2	95	2	09S425	09S425 nodularia s
442	6	1.2	67	2	093206	093206 nodularia s	515	6	1.2	95	2	09S424	09S424 nodularia s
443	6	1.2	67	2	093205	093205 nodularia s	516	6	1.2	95	2	093NN4	093NN4 nodularia s
444	6	1.2	68	5	09N626	09N626 mytilus edu	517	6	1.2	95	2	093NN2	093NN2 nodularia h
445	6	1.2	68	5	09NAU6	09NAU6 mytilus edu	518	6	1.2	95	2	09R310	09R310 nodularia s
446	6	1.2	69	12	08QWH6	08QWH6 human coxa	519	6	1.2	95	10	08RU85	08RU85 arabidopsis
447	6	1.2	70	2	08VMF0	08VMF0 pseudomonas	520	6	1.2	95	16	09L1V7	09L1V7 streptomyce
448	6	1.2	70	4	09BS22	09BS22 homo sapien	521	6	1.2	96	6	095KX1	095KX1 canis famli
449	6	1.2	70	12	09WIW0	09WIW0 human papil	522	6	1.2	96	16	092BM4	092BM4 listeria mo
450	6	1.2	71	16	034408	034408 bacillus su	523	6	1.2	96	16	08Y734	08Y734 listeria mo
451	6	1.2	72	5	09NAT8	09NAT8 mytilus edu	524	6	1.2	98	2	09RAG1	09RAG1 planktothri
452	6	1.2	72	12	09J8B1	09J8B1 spidoptera	525	6	1.2	98	16	09RWN2	09RWN2 deinococcus
453	6	1.2	72	17	0979M7	0979M7 thermoplasm	526	6	1.2	99	16	092GM5	092GM5 rickettsia
454	6	1.2	73	12	090728	090728 human papil	527	6	1.2	99	16		

528	6	1.2	99	16	P74283	P74283 synechocyst	601	128	5	O76888	O76888 drosophila
529	6	1.2	100	4	Q9H377	Q9H377 homo sapien	602	128	6	Q8SQ46	Q8SQ46 macaca fasc
530	6	1.2	100	16	Q9A774	Q9A774 caulobacter	603	128	6	Q8SP13	Q8SP13 macaca fasc
531	6	1.2	101	2	Q9F3Y8	Q9F3Y8 oscillatori	604	129	4	Q9H2Q1	Q9H2Q1 homo sapien
532	6	1.2	101	2	Q9F2E8	Q9F2E8 spirulina s	605	129	16	Q98K04	Q98K04 rhizobium 1
533	6	1.2	101	2	Q9F4A5	Q9F4A5 cyanobacter	606	130	2	Q9F7V9	Q9F7V9 mycobacteri
534	6	1.2	101	6	O62721	O62721 papio hamad	607	130	2	Q9KH54	Q9KH54 mycobacteri
535	6	1.2	102	5	Q9VUX2	Q9VUX2 drosophila	608	130	5	Q9TY27	Q9TY27 caenorhabdi
536	6	1.2	102	10	Q9CA51	Q9CA51 arabidopsis	609	130	10	Q9FK00	Q9FK00 arabidopsis
537	6	1.2	102	17	O28468	O28468 archaeoglob	610	130	10	Q9RX19	Q9RX19 arabidopsis
538	6	1.2	103	4	Q8XWV1	Q8XWV1 homo sapien	611	130	12	Q9IFC6	Q9IFC6 chilo iride
539	6	1.2	104	2	P95751	P95751 streptococ	612	131	13	Q98UD3	Q98UD3 xenopus lae
540	6	1.2	104	3	Q12111	Q12111 saccharomyc	613	131	17	O58137	O58137 pyrococcus
541	6	1.2	104	16	Q9KU58	Q9KU58 vibrio chol	614	132	4	Q9V3Y7	Q9V3Y7 homo sapien
542	6	1.2	105	15	Q9PXX6	Q9PXX6 bovine leuk	615	132	4	Q9ZBE1	Q9ZBE1 mycobacteri
543	6	1.2	105	16	Q8YQ72	Q8YQ72 anabaena sp	616	133	4	Q96DP7	Q96DP7 homo sapien
544	6	1.2	106	5	Q9NTQ6	Q9NTQ6 trypanosoma	617	133	5	Q9VNS5	Q9VNS5 drosophila
545	6	1.2	106	16	Q92R68	Q92R68 rhizobium m	618	133	11	Q9D2Q4	Q9D2Q4 mus musculu
546	6	1.2	107	12	Q8V559	Q8V559 monkeypox v	619	134	6	Q9BDB9	Q9BDB9 tragulus ja
547	6	1.2	108	12	O41278	O41278 strawberry	620	134	10	Q9C8P3	Q9C8P3 arabidopsis
548	6	1.2	109	11	Q9JJ47	Q9JJ47 mus musculu	621	134	12	Q918P5	Q918P5 chilli leaf
549	6	1.2	109	16	O86551	O86551 streptomyce	622	134	12	Q9YVA9	Q9YVA9 gallid herp
550	6	1.2	110	9	Q38474	Q38474 bacterioph	623	134	16	Q9PFC9	Q9PFC9 xylella fas
551	6	1.2	110	16	Q9KS03	Q9KS03 vibrio chol	624	134	16	Q9PFC9	Q9PFC9 xylella fas
552	6	1.2	110	17	O27031	O27031 methanobact	625	134	17	Q96Z34	Q96Z34 sulfolobus
553	6	1.2	110	17	Q9YDV9	Q9YDV9 aeropyrum p	626	134	17	Q8U2N1	Q8U2N1 pyrococcus
554	6	1.2	111	12	Q91CJ7	Q91CJ7 human adeno	627	135	6	Q9TS23	Q9TS23 bos taurus
555	6	1.2	111	16	Q8X4J8	Q8X4J8 escherichia	628	135	16	Q9X828	Q9X828 streptomyce
556	6	1.2	112	4	Q9UGV4	Q9UGV4 homo sapien	629	135	17	Q9V091	Q9V091 pyrococcus
557	6	1.2	112	13	Q98TN3	Q98TN3 platichthys	630	136	5	Q97374	Q97374 lymanea sta
558	6	1.2	113	15	Q9WNX3	Q9WNX3 human immun	631	136	11	Q9D355	Q9D355 mus musculu
559	6	1.2	113	16	Q98LD5	Q98LD5 rhizobium 1	632	137	2	Q9AE00	Q9AE00 agrobacteri
560	6	1.2	114	10	Q8VWS7	Q8VWS7 narcissus p	633	137	5	Q96335	Q96335 pseudomonas
561	6	1.2	114	12	Q8QWV2	Q8QWV2 hepatitis e	634	137	10	Q9FL86	Q9FL86 arabidopsis
562	6	1.2	115	8	Q955U0	Q955U0 cheirogaleu	635	137	13	Q9PVP4	Q9PVP4 agkistrodon
563	6	1.2	115	8	Q955U0	Q955U0 cheirogaleu	636	138	12	Q81447	Q81447 hepatitis c
564	6	1.2	115	8	Q94PV1	Q94PV1 cheirogaleu	637	138	16	Q9HUC2	Q9HUC2 pseudomonas
565	6	1.2	115	10	Q94N60	Q94N60 cheirogaleu	638	139	6	Q29578	Q29578 sus scrofa
566	6	1.2	115	10	Q9ZRN5	Q9ZRN5 glycyrrhiza	639	139	10	Q9C7Q5	Q9C7Q5 arabidopsis
567	6	1.2	115	16	Q9AB18	Q9AB18 caulobacter	640	139	13	Q9PVE9	Q9PVE9 agkistrodon
568	6	1.2	116	10	Q94JE6	Q94JE6 oryza sativ	641	139	16	Q9KGF3	Q9KGF3 bacillus ha
569	6	1.2	116	10	Q8W346	Q8W346 oryza sativ	642	140	8	O79662	O79662 scomber jap
570	6	1.2	116	16	Q8X2D7	Q8X2D7 escherichia	643	140	8	O79664	O79664 scomber aus
571	6	1.2	117	5	Q9VZL6	Q9VZL6 drosophila	644	140	8	Q9T613	Q9T613 scomber jap
572	6	1.2	118	10	Q9SMW1	Q9SMW1 brassica na	645	140	10	O65171	O65171 mesembryant
573	6	1.2	119	5	Q8SVR2	Q8SVR2 encephalito	646	141	10	O65171	O65171 mesembryant
574	6	1.2	119	16	Q9J787	Q9J787 neisseria m	647	141	17	Q9YB15	Q9YB15 aeropyrum p
575	6	1.2	120	5	Q8SXW8	Q8SXW8 drosophila	648	141	17	Q9HKP1	Q9HKP1 thermoplasm
576	6	1.2	120	12	Q89359	Q89359 paramecium	649	142	2	Q93SJ6	Q93SJ6 myxococcus
577	6	1.2	120	15	Q907P2	Q907P2 human immun	650	142	6	Q9BEC3	Q9BEC3 tragulus ja
578	6	1.2	121	4	Q9BWP5	Q9BWP5 homo sapien	651	142	6	Q9AD16	Q9AD16 oryza sativ
579	6	1.2	121	5	Q9U1A3	Q9U1A3 leishmania	652	142	12	Q9IRJ7	Q9IRJ7 turkey herp
580	6	1.2	121	5	Q8SVT6	Q8SVT6 encephalito	653	142	16	Q8XZH3	Q8XZH3 ralstonia s
581	6	1.2	121	16	Q9A314	Q9A314 caulobacter	654	143	5	Q9GV87	Q9GV87 lucina pect
582	6	1.2	124	16	P74350	P74350 synechocyst	655	143	5	Q9XVB3	Q9XVB3 caenorhabdi
583	6	1.2	124	16	Q99WS4	Q99WS4 staphylococ	656	143	13	Q98TL2	Q98TL2 platichthys
584	6	1.2	124	17	O28114	O28114 archaeoglob	657	144	2	Q93DY3	Q93DY3 magnetospir
585	6	1.2	124	17	Q9HCT3	Q9HCT3 halobacteri	658	144	6	Q9BH14	Q9BH14 antilocapra
586	6	1.2	125	8	Q9T612	Q9T612 scomber aus	659	144	9	Q9AMV8	Q9AMV8 haemophilus
587	6	1.2	125	10	Q9LNU5	Q9LNU5 arabidopsis	660	144	10	Q9MAB2	Q9MAB2 arabidopsis
588	6	1.2	125	16	Q8XXH6	Q8XXH6 ralstonia s	661	144	16	Q91738	Q91738 pseudomonas
589	6	1.2	126	1	P95985	P95985 sulfolobus	662	144	16	O8Y1P1	O8Y1P1 ralstonia s
590	6	1.2	126	4	Q96B14	Q96B14 homo sapien	663	144	17	Q9HHY6	Q9HHY6 halobacteri
591	6	1.2	126	5	O16598	O16598 caenorhabdi	664	145	2	Q9AEW4	Q9AEW4 pseudomonas
592	6	1.2	126	10	O80800	O80800 arabidopsis	665	145	2	Q38724	Q38724 allium ursi
593	6	1.2	126	16	Q9A9C3	Q9A9C3 caulobacter	666	145	10	Q9SJO8	Q9SJO8 arabidopsis
594	6	1.2	126	16	Q9RKC9	Q9RKC9 streptomyce	667	145	13	Q90YX3	Q90YX3 spirochaetes
595	6	1.2	127	5	Q90688	Q90688 culex pipie	668	146	5	O76915	O76915 drosophila
596	6	1.2	127	5	Q9U684	Q9U684 culex pipie	669	146	5	Q9VG68	Q9VG68 drosophila
597	6	1.2	127	5	Q9U675	Q9U675 culex pipie	670	147	8	Q9T9H7	Q9T9H7 halocynthia
598	6	1.2	127	8	Q9T611	Q9T611 scomber aus	671	147	10	Q8S0H7	Q8S0H7 oryza sativ
599	6	1.2	127	11	Q9DAK7	Q9DAK7 mus musculu	672	147	11	Q8VD87	Q8VD87 rattus ratt
600	6	1.2	127	16	Q9KNK3	Q9KNK3 vibrio chol	673	147	16	Q9CEM1	Q9CEM1 lactococcus

674	1.2	147	16	Q9CHX4	Q9chx4 lactococcus	747	6	1.2	158	2	Q50812	Q50812 mycobacteri
675	1.2	148	4	Q9UFX2	Q9ufx2 homo sapien	748	6	1.2	158	6	Q95ME6	Q95me6 sus scrofa
676	1.2	148	4	Q96K46	Q96k46 homo sapien	749	6	1.2	158	10	Q43759	Q43759 glycine max
677	1.2	148	10	Q9XHP1	Q9xhp1 sesamum ind	750	6	1.2	158	10	Q9FMH9	Q9fmh9 arabidopsis
678	1.2	148	10	Q8S608	Q8s608 oryza sativ	751	6	1.2	158	10	Q9SUM5	Q9sum5 arabidopsis
679	1.2	148	17	Q9FRK5	Q9frk5 aeropyrum p	752	6	1.2	158	10	Q8SIU3	Q8slu3 oryza sativ
680	1.2	149	2	Q59588	Q59588 mycobacteri	753	6	1.2	158	16	Q970A4	Q97q4 streptococc
681	1.2	149	11	Q8VD95	Q8vd95 berylmys bo	754	6	1.2	158	16	Q69527	Q69527 mycobacteri
682	1.2	149	11	Q8VD91	Q8vd91 rattus exul	755	6	1.2	158	16	Q8XZ82	Q8xz82 ralstonia s
683	1.2	149	11	Q8VD91	Q8vd91 rattus fusc	756	6	1.2	158	17	Q26301	Q26301 methanobact
684	1.2	149	11	Q8VD83	Q8vd83 sundanys mu	757	6	1.2	159	4	Q9HOM9	Q9hom9 homo sapien
685	1.2	149	11	Q8VD83	Q8vd83 sundanys mu	758	6	1.2	159	10	Q9SZY5	Q9szy5 arabidopsis
686	1.2	149	12	Q9LHN3	Q9lhn3 human polio	759	6	1.2	159	16	Q9A1Q6	Q9a1q6 streptococc
687	1.2	149	12	Q9LHN3	Q9lhn3 human polio	760	6	1.2	160	8	Q47209	Q47209 caryota mit
688	1.2	149	12	Q9LHN3	Q9lhn3 human polio	761	6	1.2	160	8	Q32197	Q32197 eichhornia
689	1.2	149	12	Q9LHN3	Q9lhn3 human polio	762	6	1.2	160	8	Q32197	Q32197 eichhornia
690	1.2	149	12	Q9LHN3	Q9lhn3 human polio	763	6	1.2	160	8	Q32197	Q32197 eichhornia
691	1.2	149	12	Q9LHN3	Q9lhn3 human polio	764	6	1.2	160	12	Q65859	Q65859 beet yellow
692	1.2	149	12	Q9LHN3	Q9lhn3 human polio	765	6	1.2	160	16	Q9KSD5	Q9ksd5 vibrio chol
693	1.2	149	17	Q9YDS5	Q9yds5 aeropyrum p	766	6	1.2	160	16	Q99VY8	Q99vy8 staphylococ
694	1.2	149	17	Q8ZWS1	Q8zws1 pyrobaculum	767	6	1.2	160	16	Q8RI73	Q8ri73 fusbacteri
695	1.2	150	1	Q9C4Q6	Q9c4q6 methanococc	768	6	1.2	161	2	Q9S412	Q9s412 actinobacill
696	1.2	150	2	Q9ZGK5	Q9zgz5 leptospira	769	6	1.2	161	10	Q9SC01	Q9sc01 tremia virga
697	1.2	150	5	Q9V3L7	Q9v3l7 drosophila	770	6	1.2	161	10	Q8I198	Q8i198 nicotiana t
698	1.2	150	8	Q33578	Q33578 trypanosoma	771	6	1.2	161	16	Q9K088	Q9k088 neisseria m
699	1.2	150	11	Q8VD94	Q8vd94 berylmys bo	772	6	1.2	161	16	Q9JY98	Q9jy98 neisseria m
700	1.2	150	11	Q8VD92	Q8vd92 rattus exul	773	6	1.2	161	16	Q8RSY9	Q8rsy9 fusbacteri
701	1.2	150	11	Q8VD88	Q8vd88 rattus norv	774	6	1.2	162	2	Q9AM02	Q9am02 synchococc
702	1.2	150	11	Q8VD86	Q8vd86 rattus ratt	775	6	1.2	162	2	Q93RE5	Q93re5 vibrio chol
703	1.2	151	4	Q9UOC1	Q9uoc1 homo sapien	776	6	1.2	162	2	Q9N119	Q9n119 callithrix
704	1.2	151	8	Q9GOK1	Q9gok1 lampsilis t	777	6	1.2	162	8	Q47176	Q47176 narcissus a
705	1.2	151	8	Q95AX4	Q95ax4 dioscorea b	778	6	1.2	162	8	Q47177	Q47177 narcissus c
706	1.2	151	16	Q9C107	Q9c107 lactococcus	779	6	1.2	162	8	Q47178	Q47178 narcissus c
707	1.2	151	16	Q8Z039	Q8z039 anabaena sp	780	6	1.2	162	8	Q47179	Q47179 narcissus r
708	1.2	151	16	Q8UGZ6	Q8ugz6 agrobacteri	781	6	1.2	162	8	Q47180	Q47180 narcissus r
709	1.2	152	6	Q8SQ10	Q8sq10 macaca neme	782	6	1.2	162	8	Q47181	Q47181 narcissus b
710	1.2	152	6	Q8SQ09	Q8sq09 papio hamad	783	6	1.2	162	8	Q47182	Q47182 narcissus c
711	1.2	152	6	Q8SPN5	Q8spn5 macaca mula	784	6	1.2	162	8	Q47183	Q47183 narcissus h
712	1.2	152	6	Q8SPF2	Q8spf2 cercopitheci	785	6	1.2	162	8	Q47184	Q47184 narcissus t
713	1.2	152	11	Q9D416	Q9d416 mus muscullu	786	6	1.2	162	8	Q47185	Q47185 narcissus t
714	1.2	152	11	Q8VD90	Q8vd90 rattus fusc	787	6	1.2	162	8	Q47186	Q47186 narcissus t
715	1.2	152	11	Q8VD89	Q8vd89 rattus norv	788	6	1.2	162	8	Q47187	Q47187 narcissus a
716	1.2	152	11	Q8VD84	Q8vd84 rattus tiom	789	6	1.2	162	8	Q47188	Q47188 narcissus f
717	1.2	153	4	Q16869	Q16869 homo sapien	790	6	1.2	162	8	Q47189	Q47189 narcissus g
718	1.2	153	8	Q94RE5	Q94re5 lithobius f	791	6	1.2	162	8	Q47190	Q47190 narcissus j
719	1.2	153	10	Q9AUD1	Q9aud1 sesamum ind	792	6	1.2	162	8	Q47191	Q47191 narcissus v
720	1.2	153	11	Q923T8	Q923t8 rattus norv	793	6	1.2	162	8	Q47192	Q47192 narcissus b
721	1.2	153	16	P77184	P77184 escherichia	794	6	1.2	162	8	Q47193	Q47193 narcissus a
722	1.2	154	12	Q916G3	Q916g3 hepatitis c	795	6	1.2	162	8	Q47194	Q47194 narcissus h
723	1.2	154	12	Q916G2	Q916g2 hepatitis c	796	6	1.2	162	8	Q47195	Q47195 narcissus i
724	1.2	154	12	Q916G0	Q916g0 hepatitis c	797	6	1.2	162	8	Q47196	Q47196 narcissus l
725	1.2	154	12	Q916F9	Q916f9 hepatitis c	798	6	1.2	162	8	Q47197	Q47197 narcissus p
726	1.2	154	12	Q9Q0D6	Q9q0d6 hepatitis c	799	6	1.2	162	8	Q47198	Q47198 narcissus r
727	1.2	154	12	Q8Q0D5	Q8q0d5 hepatitis c	800	6	1.2	162	8	Q47199	Q47199 narcissus d
728	1.2	154	12	Q8Q0D4	Q8q0d4 hepatitis c	801	6	1.2	162	8	Q47200	Q47200 narcissus e
729	1.2	154	12	Q8Q0D3	Q8q0d3 hepatitis c	802	6	1.2	162	8	Q47201	Q47201 narcissus p
730	1.2	154	12	Q8Q0D2	Q8q0d2 hepatitis c	803	6	1.2	162	8	Q47202	Q47202 narcissus t
731	1.2	154	16	Q9PCE7	Q9pce7 xylella fas	804	6	1.2	162	8	Q47203	Q47203 narcissus t
732	1.2	155	2	Q9L3Y9	Q9l3y9 staphylococ	805	6	1.2	162	8	Q47205	Q47205 leucocjum ae
733	1.2	155	6	Q8SQ08	Q8sq08 saimiri sci	806	6	1.2	162	8	Q47207	Q47207 ananas como
734	1.2	156	6	Q8SQ07	Q8sq07 saquinus oe	807	6	1.2	162	8	Q47208	Q47208 anigoantho
735	1.2	156	6	Q8SQ06	Q8sq06 ateles geof	808	6	1.2	162	8	Q32176	Q32176 eichhornia
736	1.2	156	6	Q8SQ05	Q8sq05 lagotrix i	809	6	1.2	162	8	Q32201	Q32201 eichhornia
737	1.2	156	6	Q8SQ04	Q8sq04 jamesbritte	810	6	1.2	162	8	Q32210	Q32210 eichhornia
738	1.2	156	8	Q8WH47	Q8wh47 oryza sativ	811	6	1.2	162	8	Q32390	Q32390 heteranther
739	1.2	156	13	Q73641	Q73641 fuqu rubrip	812	6	1.2	162	8	Q32400	Q32400 hydrothrix
740	1.2	156	16	Q8Z1F4	Q8z1f4 salmonella	813	6	1.2	162	8	Q32424	Q32424 heteranther
741	1.2	156	17	Q9YC18	Q9yc18 aeropyrum p	814	6	1.2	162	8	Q32430	Q32430 heteranther
742	1.2	157	2	Q8VMX2	Q8vmx2 listeria mo	815	6	1.2	162	8	Q32441	Q32441 heteranther
743	1.2	157	4	Q15614	Q15614 homo sapien	816	6	1.2	162	8	Q32556	Q32556 monochoria
744	1.2	157	5	Q9N2X7	Q9n2x7 caenorhabdi	817	6	1.2	162	8	Q32579	Q32579 monochoria
745	1.2	157	16	Q8Z351	Q8z351 salmonella	818	6	1.2	162	8	Q32588	Q32588 monochoria
746	1.2	157	17	Q8ZWR7	Q8zwr7 pyrobaculum	819	6	1.2	162	8	Q32648	Q32648 monochoria

820	6	1.2	162	8	Q32846	Q32846 phylodrum l	893	162	16	Q9XA05	Q9XA05 streptomyc
821	6	1.2	162	8	Q48289	Q48289 narcissus s	894	183	5	Q9VJ96	Q9VJ96 drosophila
822	6	1.2	162	8	Q48291	Q48291 narcissus b	895	183	13	Q9O492	Q9O492 distichodus
823	6	1.2	162	8	Q48365	Q48365 narcissus c	896	183	16	Q926K4	Q926K4 listeria in
824	6	1.2	162	16	P73165	P73165 synechocyst	897	183	16	Q8XTM6	Q8XTM6 ralstonia s
825	6	1.2	162	17	Q82XT7	Q82XT7 pyrobaculum	898	183	16	Q8XQAL	Q8XQAL ralstonia s
826	6	1.2	162	17	Q8TQT6	Q8TQT6 methanosarc	899	184	2	Q9KJL3	Q9KJL3 lactococcus
827	6	1.2	163	5	Q9BMK6	Q9BMK6 brugia mala	900	184	16	Q9A4F8	Q9A4F8 caulobacter
828	6	1.2	163	6	Q9BDC2	Q9BDC2 antilocapra	901	184	17	Q8ZXU5	Q8ZXU5 pyrobaculum
829	6	1.2	163	16	Q986D1	Q986D1 rhizobium l	902	185	5	Q96380	Q96380 echinococcu
830	6	1.2	163	16	Q9RV22	Q9RV22 deinococcus	903	185	5	Q25329	Q25329 leishmania
831	6	1.2	164	2	Q30747	Q30747 rhodobacter	904	185	5	Q90977	Q90977 caenorhabdi
832	6	1.2	164	2	Q8TRR0	Q8TRR0 pseudomonas	905	185	5	Q97161	Q97161 schistosoma
833	6	1.2	164	8	Q95AX2	Q95AX2 hangana ma	906	185	5	Q9W3S3	Q9W3S3 drosophila
834	6	1.2	164	17	Q8TLC5	Q8TLC5 methanosarc	907	185	10	Q9SVQ7	Q9SVQ7 arabidopsis
835	6	1.2	165	10	Q9SIT8	Q9SIT8 arabidopsis	908	186	12	Q9IXI1	Q9IXI1 heparitis c
836	6	1.2	165	10	Q98196	Q98196 nicotiana t	909	186	17	Q9YFK4	Q9YFK4 aeropyrum p
837	6	1.2	165	10	Q9C775	Q9C775 arabidopsis	910	187	4	Q92531	Q92531 homo sapien
838	6	1.2	165	10	Q8S3Y9	Q8S3Y9 sorghum bic	911	187	10	Q94D45	Q94D45 oryza sativ
839	6	1.2	166	2	Q93M08	Q93M08 streptomyc	912	187	17	Q8T283	Q8T283 methanopyru
840	6	1.2	166	4	Q96CY7	Q96CY7 homo sapien	913	188	10	Q9FMV6	Q9FMV6 arabidopsis
841	6	1.2	166	10	Q9LR09	Q9LR09 arabidopsis	914	188	2	Q9K429	Q9K429 mycoplasma
842	6	1.2	166	17	Q9YBY4	Q9YBY4 aeropyrum p	915	189	17	Q27361	Q27361 methanobact
843	6	1.2	167	16	Q9I325	Q9I325 pseudomonas	916	189	17	Q29411	Q29411 archaeoglob
844	6	1.2	167	17	Q58561	Q58561 methanococc	917	190	2	Q9ANC2	Q9ANC2 bradyrhizob
845	6	1.2	168	2	Q30528	Q30528 pseudomonas	918	190	5	Q9U9B4	Q9U9B4 mytilus edu
846	6	1.2	168	16	Q922E0	Q922E0 rhizobium m	919	190	10	Q942Y4	Q942Y4 oryza sativ
847	6	1.2	168	16	Q83512	Q83512 treponema p	920	190	12	Q99FV8	Q99FV8 human echov
848	6	1.2	168	16	Q8VIX9	Q8VIX9 ralstonia s	921	190	16	Q9KFX1	Q9KFX1 bacillus ha
849	6	1.2	169	4	Q9H5D8	Q9H5D8 homo sapien	922	191	2	Q86058	Q86058 azospirillu
850	6	1.2	169	5	Q95S08	Q95S08 drosophila	923	191	16	Q9AC28	Q9AC28 caulobacter
851	6	1.2	169	11	Q9D0P9	Q9D0P9 mus musculu	924	191	16	Q92NR0	Q92NR0 rhizobium m
852	6	1.2	169	16	Q82MT7	Q82MT7 salmonella	925	192	3	Q74887	Q74887 schizosacch
853	6	1.2	169	16	Q9KZA3	Q9KZA3 streptomyc	926	192	5	Q9XYV6	Q9XYV6 leishmania
854	6	1.2	170	5	Q8T1H6	Q8T1H6 dictyosteli	927	192	5	Q9VQ17	Q9VQ17 drosophila
855	6	1.2	170	6	Q9BEC1	Q9BEC1 tragus ja	928	192	10	Q9FJZ8	Q9FJZ8 arabidopsis
856	6	1.2	170	8	Q953M7	Q953M7 echinococcu	929	192	17	Q58289	Q58289 pyrococcus
857	6	1.2	170	10	Q9M0Q6	Q9M0Q6 arabidopsis	930	193	5	Q8T6C4	Q8T6C4 echinococcu
858	6	1.2	170	11	Q8R3S7	Q8R3S7 mus musculu	931	193	16	Q92CZ1	Q92CZ1 listeria in
859	6	1.2	172	6	Q9BDZ0	Q9BDZ0 macaca mula	932	193	16	Q8Y879	Q8Y879 listeria mo
860	6	1.2	172	12	P89250	P89250 western equ	933	194	2	Q9K428	Q9K428 mycoplasma
861	6	1.2	172	16	Q9RT56	Q9RT56 deinococcus	934	194	10	Q9FNG5	Q9FNG5 arabidopsis
862	6	1.2	172	17	Q30098	Q30098 archaeoglob	935	194	10	Q9SD84	Q9SD84 arabidopsis
863	6	1.2	173	16	Q9RJ35	Q9RJ35 streptomyc	936	195	10	Q9LW68	Q9LW68 arabidopsis
864	6	1.2	174	8	Q9ME78	Q9ME78 drosophila	937	196	2	Q9X620	Q9X620 arabidopsis
865	6	1.2	174	8	Q9MD81	Q9MD81 drosophila	938	196	10	Q82605	Q82605 arabidopsis
866	6	1.2	174	8	Q9MG55	Q9MG55 drosophila	939	196	12	Q56371	Q56371 grapevine l
867	6	1.2	175	10	Q9S718	Q9S718 arabidopsis	940	196	16	Q8ZJR2	Q8ZJR2 versinia pe
868	6	1.2	175	11	Q8R4W8	Q8R4W8 mus musculu	941	196	17	Q97YV7	Q97YV7 sulfolobus
869	6	1.2	175	12	Q9YS39	Q9YS39 lactate deh	942	197	8	Q9T5T1	Q9T5T1 potamilus i
870	6	1.2	175	12	Q96500	Q96500 lactate deh	943	197	8	Q8WCR6	Q8WCR6 lampsis a
871	6	1.2	175	13	Q91140	Q91140 nannobrycon	944	197	8	Q8WCR5	Q8WCR5 lampsis a
872	6	1.2	175	16	Q98IT9	Q98IT9 rhizobium l	945	197	8	Q8WC05	Q8WC05 villosa vil
873	6	1.2	176	10	Q8S524	Q8S524 oryza sativ	946	197	8	Q8WCQ4	Q8WCQ4 liquimia rec
874	6	1.2	176	10	Q8S2E2	Q8S2E2 oryza sativ	947	197	8	Q8WCQ1	Q8WCQ1 lampsis t
875	6	1.2	176	16	Q9JRC8	Q9JRC8 neisseria m	948	197	12	Q56372	Q56372 grapevine l
876	6	1.2	176	16	Q9JRC8	Q9JRC8 neisseria m	949	197	13	Q98TR5	Q98TR5 fugu rubrip
877	6	1.2	177	2	Q9FT08	Q9FT08 deinococcus	950	197	16	Q99YA7	Q99YA7 streptococc
878	6	1.2	177	5	Q20598	Q20598 carboxydoth	951	197	17	Q9YCA9	Q9YCA9 aeropyrum p
879	6	1.2	177	16	Q98F69	Q98F69 caenorhabdi	952	198	2	Q9K4V7	Q9K4V7 mycoplasma
880	6	1.2	178	16	Q84475	Q84475 chlamydia t	953	198	3	Q9K4V7	Q9K4V7 mycoplasma
881	6	1.2	178	16	Q9A2V3	Q9A2V3 caulobacter	954	198	3	Q22754	Q22754 saccharomyc
882	6	1.2	178	17	Q978Q0	Q978Q0 thermoplas	955	198	11	Q8SX04	Q8SX04 drosophila
883	6	1.2	179	5	Q9VX88	Q9VX88 drosophila	956	198	16	Q61861	Q61861 mus musculu
884	6	1.2	179	5	Q9VDH9	Q9VDH9 drosophila	957	198	16	Q9RSV1	Q9RSV1 deinococcus
885	6	1.2	180	5	Q9NE73	Q9NE73 leishmania	958	199	2	Q68985	Q68985 streptomyc
886	6	1.2	180	10	Q9LRO6	Q9LRO6 arabidopsis	959	199	2	Q68985	Q68985 chlorobium
887	6	1.2	180	16	Q92C81	Q92C81 listeria in	960	199	5	Q16026	Q16026 dirofilaria
888	6	1.2	180	17	Q8TTD3	Q8TTD3 methanosarc	961	199	5	Q9Y082	Q9Y082 globodera r
889	6	1.2	181	10	Q49177	Q49177 oryza sativ	962	199	6	Q9BG14	Q9BG14 bos taurus
890	6	1.2	182	10	Q8S526	Q8S526 oryza sativ	963	199	8	Q99503	Q99503 potamilus i
891	6	1.2	182	10	Q8S655	Q8S655 oryza sativ	964	199	8	Q99505	Q99505 potamilus p
892	6	1.2	182	16	Q9HTN6	Q9HTN6 pseudomonas	965	199	8	Q99507	Q99507 potamilus a

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966 6 1.2 199 8 099508 099508 potamilus o
967 6 1.2 199 8 099509 099509 potamilus a
968 6 1.2 199 8 099510 099510 potamilus a
969 6 1.2 199 8 099511 099511 leucocoea fr
970 6 1.2 199 8 099514 099514 leucocoea c
971 6 1.2 199 8 099514 099514 leucocoea c
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1000 6 1.2 201 4 099520 099520 homo sapien

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ALIGNMENTS

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RESULT 1
ID Q9HCT9 PRELIMINARY; PRT: 500 AA.
AC Q9HCT9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
DE precursor).
GN TEM7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lal A., Riggins G.G., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA St Croix B., Vogelstein B., Kinzler K.W.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";

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RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF279144; AAL00869.2; -.
DR EMBL; AF378753; AAL1190.1; -.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF01437; PSI; 1.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00539; NIDO; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;

Query Match 100.0%; Score 500; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTIVRGWNRRAESPFGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTIVRGWNRRAESPFGHVSEPD 60
QY 61 TOLSDGLGGTILMDTLDPNTRVVDNHSYVSVLYGSPHSEPHSLVVDVAEANRSQVK 120
Db 61 TOLSDGLGGTILMDTLDPNTRVVDNHSYVSVLYGSPHSEPHSLVVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 180
Db 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 180
QY 181 NFNPQYSDNSIVVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPQYSDNSIVVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPETSSQHPVKTGSLDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
Db 241 SVPETSSQHPVKTGSLDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACSSDLTFNCNCHVLQRCSSGDFRYRQEMDMYGCQAEGRMCDQ 360
Db 301 LPTCLQHRSCDACSSDLTFNCNCHVLQRCSSGDFRYRQEMDMYGCQAEGRMCDQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTDEDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTDEDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVEPSGHEKEGFMFAEQC 500
Db 481 YAEVEPSGHEKEGFMFAEQC 500

RESULT 2
Q9CWV5 PRELIMINARY; PRT: 500 AA.
ID Q9CWV5;
AC Q9CWV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 2410003107RIK protein.
GN 2410003107RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010361; BAB26881.1; -;
DR MGD; MGI:1919574; 2410003107Rik.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;

Query Match 7.0%; Score 35; DB 11; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HQASRVLSFDPPFYGHPLRQITATGCFIFMGD 163
DB 130 HQASRVLSFDPPFYGHPLRQITATGCFIFMGD 164

RESULT 3
Q912V7 PRELIMINARY; PRT; 500 AA.
ID Q912V7
AC Q912V7
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor.
GN 2410003107Rik OR TM7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378760; AAL11997.1; -;
DR MGD; MGI:1919574; 2410003107Rik.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 500 TUMOR ENDOTHELIAL MARKER 7.
SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;

Query Match 7.0%; Score 35; DB 11; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HQASRVLSFDPPFYGHPLRQITATGCFIFMGD 163

DB 130 HQASRVLSFDPPFYGHPLRQITATGCFIFMGD 164
RESULT 4
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ID Q96E59
AC Q96E59
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1200007L24 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012885; AAL12885.1; -;
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
SQ SEQUENCE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 2.0%; Score 10; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDPPFYGH 146
DB 112 LSFDPPFYGH 121

RESULT 5
Q96PD9 PRELIMINARY; PRT; 529 AA.
ID Q96PD9
AC Q96PD9
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN TM7R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378757; AAL11994.1; -;
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
KW Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 529 TUMOR ENDOTHELIAL MARKER 7-RELATED.
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 2.0%; Score 10; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDPPFYGH 146
DB 161 LSFDPPFYGH 170

RESULT 6

Q9DC11 ID Q9DC11 PRELIMINARY; PRT; 530 AA.
 AC Q9DC11;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 1200007L24RIK protein.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=LUNG;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK004640; BAB23431.1;
 DR MGD: MGI:1914698; 1200007L24RIK.
 DR InterPro: IPR003886; Nidogen_ext.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002165; plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 DR SMART: SM00539; NIDO: 1.
 DR SMART: SM00423; PSI: 1.
 SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 2.0%; Score 10; DB 11; Length 530;
 Best Local Similarity 100.0%; Pred. No. 0.44;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
 DB 161 LSFDFPFYGH 170

RESULT 7

Q91ZV6 ID Q91ZV6 PRELIMINARY; PRT; 530 AA.
 AC Q91ZV6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Tumor endothelial marker 7-related precursor.
 GN 1200007L24RIK OR TEM7R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC MEDLINE=21443268; PubMed=11559528;
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,

RA Kinzler K.W., St Croix B.;
 RT "Cell surface tumor endothelial markers are conserved in mice and humans."
 RL Cancer Res. 61:6649-6655(2001).
 DR EMBL: AF378761; AAL11998.1;
 DR MGD: MGI:1914698; 1200007L24RIK.
 DR InterPro: IPR002165; plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 KW Signal.
 FT SIGNAL. 1 30 POTENTIAL.
 FT CHAIN 31 530 TUMOR ENDOTHELIAL MARKER 7-RELATED.
 SQ SEQUENCE 530 AA; 59625 MW; FF9315020735E36D CRC64;

Query Match 2.0%; Score 10; DB 11; Length 530;
 Best Local Similarity 100.0%; Pred. No. 0.44;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
 DB 161 LSFDFPFYGH 170

RESULT 8

P94476 ID P94476 PRELIMINARY; PRT; 655 AA.
 AC P94476;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE YEB.
 GN Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 TRPC2;
 RX MEDLINE=88011308; PubMed=2821284;
 RA Donovan W., Zheng L.B., Sandman K., Losick R.;
 RT "Genes encoding spore coat polypeptides from Bacillus subtilis."
 RL J. Mol. Biol. 196:1-10(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 TRPC2;
 RA Wray L., Person A., Fisher S.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 TRPC2;
 RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Madique C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche M., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U51115; AB62310.1; -;
 DR EMBL: Z99107; CAB12454.1; -;
 DR IPR002931; Trnsglutase_like.
 DR Pfam: PF01841; Transglut_core; 1.
 DR SMART: SM00460; TGC; 1.
 KW Complete proteome.
 SQ SEQUENCE 655 AA; 75361 MW; 74ECF63B9E1E72CA CRC64;

Query Match 1.8%; Score 9; DB 16; Length 655;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 VLAVLLVAA 439
 Db 565 VLAVLLVAA 573

RESULT 9
 Q97019 PRELIMINARY; PRT; 208 AA.
 AC Q97019;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein ST1606.
 GN ST1606.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT *Crenarchaeon*, *Sulfolobus tokodaii* strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AF000987; BAB66684.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 208 AA; 23192 MW; D8C1DEDFE407BD9A CRC64;

Query Match 1.6%; Score 8; DB 17; Length 208;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 LLVAAIIL 442
 Db 67 LLVAAIIL 74

RESULT 10
 Q9S2F8 PRELIMINARY; PRT; 224 AA.
 AC Q9S2F8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein SCO2923.
 GN SCO2923 OR SCE19.23C.
 DN Streptomyces coelicolor.
 OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL096852; CAB51004.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 224 AA; 23496 MW; 619CCAE7C8CF7A8B CRC64;

Query Match 1.6%; Score 8; DB 16; Length 224;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 GIVLAVLL 436
 Db 132 GIVLAVLL 139

RESULT 11
 Q54303 PRELIMINARY; PRT; 317 AA.
 ID Q54303
 AC Q54303;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Methyltransferase.
 GN RAPM.
 OS Streptomyces hygroscopicus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 5491;
 RX MEDLINE=95372374; PubMed=7644502;
 RA Schwecke T., Aparicio J.F., Molnar I., Koenig A., Khaw L.E.,
 RA Haydock S.F., Ollinyk M., Caffrey P., Cortes J., Lester J.B.,
 RA Boehm G.A., Staunton J., Leadlay P.F.;
 RT "The biosynthetic gene cluster for the polyketide immunosuppressant
 RT rapamycin.";
 RL proc. Natl. Acad. Sci. U.S.A. 92:7839-7843(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 5491;
 RX MEDLINE=96186895; PubMed=8635730;
 RA Molnar I., Aparicio J.F., Haydock S.F., Khaw L.E., Schwecke T.,
 RA Koenig A., Staunton J., Leadlay P.F.;
 RT "Organisation of the biosynthetic gene cluster for rapamycin in

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RT Streptomyces hygroscopicus: analysis of genes flanking the polyketide
RT synthase."
RL Gene 169:1-7(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 5491;
RX MEDLINE=961186896; PubMed=8635756;
RA Aparicio J.F., Molnar I., Schwecke T., Koenig A., Haydock S.F.,
RA Khaw L.E., Staunton J., Leadlay P.F., Staunton J., Leadlay P.F.;
RT "Organization of the biosynthetic gene cluster for rapamycin in
RT Streptomyces hygroscopicus: analysis of the enzymatic domains in the
RT modular polyketide synthase.";
RL Gene 169:9-16(1996).
DR EMBL; X86780; CAA60466.1; -.
DR InterPro; IPR000051; SAM_bind.
KW Transferase.
SQ SEQUENCE 317 AA; 35065 MW; 42F6A477FDAC0011 CRC64;

Query Match 1.6%; Score 8; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LREAARAL 19
DB 188 LREAARAL 195
|||||

RESULT 12
Q9HQA6 PRELIMINARY; PRT; 363 AA.
AC Q9HQA6
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Vng1250h.
GN VNG1250H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonksi P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RW EMBL; AE005050; AAG19609.1; -.
KW Complete proteome.
SQ SEQUENCE 363 AA; 37543 MW; A1CD167FA482ABED CRC64;

Query Match 1.6%; Score 8; DB 17; Length 363;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 LAVLLVAA 439
DB 17 LAVLLVAA 24
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RESULT 13
Q9AC73 PRELIMINARY; PRT; 429 AA.
AC Q9AC73
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Pros176.
GN PROS176.
OS Neisseria meningitidis serogroup B strain
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy K., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RW EMBL; AE002515; AAF41996.1; -.
KW TIGR; NMB1647; -.
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR001463; Na/Ala_symptr.
DR Pfam; PF01235; Na/Ala_symp.
DR PRINTS; PR00175; NAALASMPORT.
DR TIGRFAMS; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.

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DE Arsenic efflux pump protein.
GN ARSB OR SAP017.
OS Staphylococcus aureus (strain N315).
OG Plasmid pN315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RW EMBL; AP003139; BAB43886.1; -.
DR InterPro; IPR000802; Ars_pump.
DR Pfam; PF02040; Arsb; 1.
DR PRINTS; PR00758; ARSENICPUMP.
DR TIGRFAMS; TIGR00935; 2a45; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 429 AA; 46469 MW; 654CFB2A1C9A0ADB CRC64;

Query Match 1.6%; Score 8; DB 16; Length 429;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 IVLAVLLV 437
DB 230 IVLAVLLV 237
|||||

RESULT 14
Q9JYC8 PRELIMINARY; PRT; 472 AA.
AC Q9JYC8
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Amino acid symporter, putative.
GN NMB1647.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy K., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RW EMBL; AE002515; AAF41996.1; -.
KW TIGR; NMB1647; -.
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR001463; Na/Ala_symptr.
DR Pfam; PF01235; Na/Ala_symp.
DR PRINTS; PR00175; NAALASMPORT.
DR TIGRFAMS; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.

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SQ SEQUENCE 472 AA; 50465 MW; 6EAD257B41C7D68F CRC64;

Query Match 1.6%; Score 8; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIIVLAVL 435

Db 195 VGIIVLAVL 202

RESULT 15

Q9JTB1
ID Q9JTB1 PRELIMINARY; PRT; 472 AA..
AC Q9JTB1; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative sodium:alanine symporter.
GN NMA1901
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85122.1;
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR001463; Na/Ala_symptr.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR PRINTS; PR00175; NAALASMPOR.
DR TIGRFAMs; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 472 AA; 50457 MW; 6FELD6BC5DB68694 CRC64;

Query Match 1.6%; Score 8; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIIVLAVL 435

Db 195 VGIIVLAVL 202

Search completed: April 22, 2003, 16:18:52
Job time : 118 secs

